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; LENGTH: 825
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-033-190-1
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TITLE OF INVENTION: IDENTIFICATION AND CHARA
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EP01-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
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AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANT
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Publication No. US20020133848A1
GENERAL INFORMATION:
APPLICANY: Exclixis Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARA
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EPO1-002C
CURRENT FILING DATE: 2001-10-29
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
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(ANT)

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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Fang, Yiwen
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Fac
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 45
LENGTH: 1236
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US-10-021-811-45
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                                                           FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: (519)
NAME/KEY: unsure
'``"TION: (521)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/10021811 Publication No. US20030024007A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
   NAME/KEY: unsure
LOCATION: (530)..
NAME/KEY: unsure
LOCATION: (534)
                                                                                                                                                         ORGANISM: Glycine
                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTCTCTTAATTTACCACCCATGCAACAAGGAGTACAAAATGATGATTTTTCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGTCATGAAAATTGGGGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTGCAAGGAAATAATAAGTGAGAAACAAACTCCAGATGCATCGATGGACAACGTAGAT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTTCTCAAGCACAATGAAGAATGTTACAAACAATAATGTAATTTTGGACGAGGAGGAA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAACACTAATCTTCTAAGGAAGTTAAATACTACTACTACTACTCCTCCCCGAAAAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGGTCACTTATTGCTGGTAGACTTCCCGGGAAGGACAGCTAACGATGTGAAAAACTAT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGTCATGAAAATTGGGGTGAA 738
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                                       . (531)
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                                                RESULT 5
US-10-021-811-43
; Sequence 43, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
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Best Local Similarity
Watches 23; Conserve
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; LOCATION: (168)..(1196)
; OTHER INFORMATION: G1640
US-09-934-455-251
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US-10-021-811-45
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Best Local Similarity
Matches 23; Conserv
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SEQ ID NO 251
LENGTH: 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cahoon, Reber
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
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LOCATION:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                             423
                                                                                                                                                                                                253 GGCAACAGATGGTCACTTATTGC 275
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: (800)
: unsure
: (1124)
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Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
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Yu, Guo-Liang
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Ratcliffe, Oliver
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o. US20030121070A1
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                                       Rebecca E.
                                                                                                                                                                                                                                                              100.0%;
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0.52;
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0.52;
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                                                                                                                                                                                                                                                                              Length 1300;
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US-09-878-574-2454
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                                                                                                                                                                                                                          RESULT 7
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Best Local Similarity
Matches 23; Conserv
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SEQ ID NO 43
LENGTH: 1348
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CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
                                                                                                                                              Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
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Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(390)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-024-Q1-B1-G6
-09-878-574-2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
             APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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FILING DATE: 2000-08-23
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PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/487,429 PRIOR FILING DATE: 1995-06-07
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FEATURE:

NAME/KEY: misc feature

FEATURE:

(36551)...(36
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NAME/KEY: misc_feature

*OCATION: (47036)..(47036)

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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (45732)...(45732)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals
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LOCATION: (44905)...(44905)
OTHER INFORMATION: n equals
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LOCATION: (44416)...(44416)
OTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (36543)...(36543)
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OTHER INFORMATION: n equals
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LOCATION: (9921)..(992
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ORGANISM: Haemophilus influenzae
                                         LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
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LOCATION: (36636)..(36636)
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LOCATION: (29298)..(29298)
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NAME/KEY: misc_feature
LOCATION: (51602)..(51602)
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NAME/KEY: misc feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
                                            NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (119750)..(119750)
DTHER_INFORMATION: n equals
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LOCATION: (102696)..(102696)
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LOCATION: (80024)..(80024)
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LOCATION: (65313)..(65313)
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OCATION: (120038)...(120038)
NTHER INFORMATION: n equals
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OCATION: (117136)..(117136)
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.OCATION: (105121)..(105121)
.THER INFORMATION: n equals a,
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LOCATION: (51786)..(51
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OCATION: (107248)..(1
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR APPLICATION NUMBER: US/09/938,842A
PRIOR APPLICATION NUMBER: US/09/938,842A
PRIOR APPLICATION NUMBER: US/09/938,842A
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                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                               Sequence 121, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
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LOCATION: (145058)..(145058)
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LOCATION: (140398)..(140398)
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NAME/KEY: misc feature
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LOCATION: (145171)..(1
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LOCATION: (142750)..(142750)
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                             US-10-369-493-24702
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; TYPE: DNA
; ORGANIZM: Arabidopsis thaliana
US-09-938-842A-121
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SEQ ID NO 121
LENGTH: 741
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Publication No.
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Best Local
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SEQ ID NO 121
                                    SEQ ID NO 24702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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TYPE: DNA
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APPLICATION NUMBER: US 60/264,647
FILING DATE: 2001-01-16
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100.0%; Pred. No.
tive 0; Mismatc
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US-10-098-263B-91990
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; ORGANISM: Human
US-10-027-632-31145
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SOFTWARE: Microarray Probe S
SEQ ID NO 91990
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Best Local Similarity
Matches 20; Conserv
                                                                              SOFTWARE: FASTSEQ
SEQ ID NO 31145
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Matches 19; Conservative (
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PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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CURRENT FILING DATE: 2003-01-08
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TITLE OF INVENTION: Human Microarray
                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                        PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                        RIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                  RIOR FILING DATE: 2000-03-29
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                                                          LENGTH: 966
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18;
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US-10-027-632-31145
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local :
                                                                        PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                     CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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820 14 1.7 993 821 14 1.7 993 822 14 1.7 993 823 14 1.7 993 824 14 1.7 993 825 14 1.7 993 826 14 1.7 1000 827 14 1.7 1001 828 14 1.7 1001 829 14 1.7 1001 829 14 1.7 1001 820 14 1.7 1001	14 1.7 993 14 1.7 993	793 14 1.7 966 794 14 1.7 966 795 14 1.7 969 796 14 1.7 969 797 14 1.7 978 798 14 1.7 979 800 14 1.7 979 800 14 1.7 979 801 14 1.7 987 803 14 1.7 987 803 14 1.7 987 804 14 1.7 990 805 14 1.7 990 806 14 1.7 990 807 14 1.7 990 808 14 1.7 990 808 14 1.7 990 809 14 1.7 990 809 14 1.7 990	763 14 1.7 859 764 14 1.7 867 765 14 1.7 867 766 14 1.7 867 767 14 1.7 867 769 14 1.7 867 770 14 1.7 879 771 14 1.7 879 772 14 1.7 879 773 14 1.7 897 775 14 1.7 907 776 14 1.7 907 777 14 1.7 909 778 14 1.7 909 779 14 1.7 925 781 14 1.7 949 782 14 1.7 925 782 14 1.7 949 783 14 1.7 949 784 14 1.7 949 785 14 1.7 949 786 14 1.7 949 787 14 1.7 949 788 14 1.7 949 788 14 1.7 949 788 14 1.7 949 789 14 1.7 949 789 14 1.7 949 789 14 1.7 949 789 14 1.7 949 789 14 1.7 957 790 14 1.7 957	758 14 1.7 841 759 14 1.7 841 760 14 1.7 852 761 14 1.7 852 762 14 1.7 858
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1.7	1.7	1.7 1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7 1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
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1434 4 US-09-328-352-1302 1435 2 US-08-955-713-3 1437 4 US-09-107-532A-1268 1442 4 US-08-833-752-3	2 4 4 9	3 4 1 3 US	111	111	111	1 1 4	4 4 US	4 4 c	 	3 4	4 4 4	3 U G	* 2 4 Oq 2	3 4	3 US	3 US	4 4 US	4 US	2 4 08	4 4 S	2 US	 	2 US	4 4 US	4 3 U	4 4	4 4 US	4 4 200	3 US	3 4 US	4 US	us r

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Patent No. 6506581
GENERAL INFORMATION:
GENERAL INFORMATION: The Nucleotide sequence of
TITLE OF INVENTION: The Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  986
988
989
                                                                          TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                          APPLICATION NUMBER: 08/476,102 FILING DATE: JUN-5-1995
                                                                                                                                                                                                                                                                                                                                                                         STATE: MD
                         TOPOLOGY: linear
                                                LENGTH: 1830121 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rockville
                                                                                                                TELEPHONE: 301-309-8504
             DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   20850
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US-09-482-273-33
US-08-185-828A-11
US-09-016-434-775
US-09-134-001C-1653
US-08-714-918-82
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US-09-134-001C-1824

US-09-252-991A-11439

US-08-660-347-1

US-09-413-574-1
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US-09-134-001C-989
US-08-833-752-2
US-09-107-532A-3408
US-09-107-532A-3408
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US-09-328-352-3977
US-09-484-970B-140
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US-09-266-417-82
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US-08-185-828A-22
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218, App
3977, Ap
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GENERAL INFORMATION:
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Best Local S
                                                                   Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                      TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
1174328
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                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVET
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P10
TELECOMMUNICATION INFORMATION:
                                                                  Local Similarity 100 nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robert D.
                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO:
                                 788
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                     TTTCTGCTGAAATTGACTTAT 808
 TTTCTGCTGAAATTGACTTAT 1174308
                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Dell Pentium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3 1/2 inch diskette
                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                       LENGTH: 1830121 base pairs
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Hamilton O. Smith
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k; Pred. No. 0.5
0; Mismatches
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                                                                                   Score 21; DB 4;
Pred. No. 0.54;
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                                                                     Mismatches
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0.54;
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                                                                                                   Length 1830121;
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RESULT 3 US-09-453-702B-30 ; Sequence 30, Application US/09453702B

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RESULT 4
US-09-212-247C-1/c
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GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09212247C Patent No. 6391603 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                 APPLICANT: POMPEJUS, Markus; SUELBERGER, Harald; JOEFFKEN, Hans Wolfgang; DOVAL, Jose Luis Revuelta; JIMENEZ, Alberto; and GARCIA, Maria Angeles Santos
TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use thereof in microbial riboflavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 53701-2113
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                612 GGTTCATGGACTGATGAAG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GGTTCATGGACTGATGAAG 58
STATE: D.C.
COUNTRY: USA
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%; Score 19; DB 4; ilarity 100.0%; Pred. No. 7.5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burland,
Parna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plunkett, Guy
Welch, Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (608) 251-5000
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                                                                                                                                                                    synthesis
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836 ATTGAAGAAGATGAAGAG 853

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CURRENT APPLICATION NUMBER: US/09/699,266A
CURRENT FILLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PCT/US99/08385
PRIOR FILLING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/083,212
PRIOR FILLING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 999
TYPE: DNA
CORGANISM: Triticum aestivum
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                                                                                                          US-09-699-266A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-699-266A-5
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                                      Matches
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                                                      Best
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09699266A Patent No. 6559354
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ma, Hongchang
APPLICANT: Morakinyo, Layo O.
APPLICANT: Odell, Joan T.
APPLICANT: Orozeco Jr., Emil |
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Orozsco Jr., Emil M.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVESTION: TRANSCRIPTION AND GENE EXPRESSION REGULATORS
FILE REFERENCE: BB1164 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1911 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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APPLICATION NUMBER: US/09/212,247C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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   598 ATTGAAGAAGATGAAGAG 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 AAGGAGTACAAAATGATGA 229
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                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM AT-compatible, Pentium processor OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect version 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; Score 19; DB 4; ilarity 100.0%; Pred. No. 7.4; Conservative 0; Mismatches
                                      Conservative
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626..1582
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                                                     2.2%; Score 18;
100.0%; Pred. No.
                                    0,
                                      Mismatches
                                                      DB 4;
23;
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                                                                   Length 999;
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                                  Gaps
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APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIGMENT
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: SALKINS.003C1
CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEG ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 1033
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09610185C Patent No. 6573432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08928941D Patent No. 6180763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT: Xia, Yiji
APPLICANT: Dixon, Richard APPLICANT: Lamb, Christoph
                                                                              TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATOR OF THE PC-DOS/MS-DOS
                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,941D FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hirai, Hiroshi
APPLICANT: Sherr, Charles
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
TITLE OF INVENTION: THEREOF
LENGTH: 376, LENGTH: 376, Length: acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
Local Similarity 100.0%; F
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New Jersey
                                  3767 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 Hackensack Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                   201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Esq.
Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Query Match
Best Local Similarity
Marches 18; Conserva
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                                                                                                                        ; ORIGINAL SOURCE:
; ORGANISM: Hon
US-08-928-941D-30
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                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 134
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CU
                                                                                                                                                                    MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3767 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hirai, Hiroshi
APPLICANT: Sherr, Charles
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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2620 TGAAGAGGTTGTAATTAA 2603
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                             609 TGAAGAGGTTGTAATTAA 626
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18; Conserv
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                                                                                                                                                                                                                                                 3767 base pairs
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                                                            Conservative
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                                                                           100.0%;
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ER: 1340-1-002 N CIP
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                                                                            Score 18;
Pred. No.
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                                                               Mismatches
                                                                            DB 3;
21;
                                                                                           Length 3767;
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RESULT 9 US-09-280-590A-28/c

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RESULT 10
US-09-280-590A-30/c
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                                                                                                                                                                                                                                                 Sequence 30, Application US/09280590A Patent No. 6303772 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09280590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.2%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PATENTIA PC-DOS/MS-DOS

SOFTWARE: PATENTIA PC-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/280,590A

FILING DATE: 29-Mar-1999

CINCIPILATION - 1-1-1-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
ORIGINAL SOURCE
ORGANISM: Homo mapiens
ORGANISM: Homo mapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
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TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
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                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                             APPLICANT: Hirai, Hiroshi
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                                                                                                      NUMBER OF SEQUENCES: 46
                                                                                                                                           TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                       609 TGAAGAGGTTGTAATTAA 626
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                                    STREET: 411 Hackensack Ave, Continental Plaza, 4th
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LENGTH: 3767 base pairs
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Kazushi
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                                                        RESULT 12
US-08-926-842B-11/c
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                   Sequence 11, Application US/08926842B Patent No. 6030807
GENERAL INFORMATION:
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; ORGANISM: Acinetobacter baumannii US-09-328-352-1695
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                                                                                                                                                                           FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1695
LENGTH: 7515
TYPE: DNA
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1695, Application US/09328352 Patent No. 6562958
                                                                    Query Match
Best Local Similarity
Matches 18; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
RAPPLICATION DATA:
APPLICATION UNMER: US/09/280,590A
FILING DATE: 29-Mar-199
CLASSIFICATION: CURKNOWN'S
ATTORNEY/AGENT INFORMATION:
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les 18; Conserv
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ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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5008 AAGTTAAATACTACTAAA 5025
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                        340 AAGTTAAATACTACTAAA 357
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STRANDEDNESS: single
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Pred. No.
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TELEX: 133521
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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LOCATION:
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LOCATION:
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LOCATION:
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SOFTWARE: Patentl
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NAME/KEY:
                        OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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VENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
CDS
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                                                                                                                      ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1167
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US-09-328-352-1167
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 3555
                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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APPLICANT: Lalgudi, Ra
APPLICANT: Ito, Laura
APPLICANT: Sherman, Br
                                                                                                                                                                NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1167
LENGTH: 750
                                                                                                                                                                                                                                                                                                                       Sequence 1167, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3585, Approximately Patent No. 647621
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Best Local Similarity
Matches 18; Conserv
                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: 166-184
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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17; Conserv
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VENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
NCE: PL-0017 US
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Sequence 7, Application US/08753007A

Patent No. 6074941

GENERAL INFORMATION:

APPLICANT: Geating, David P.

APPLICANT: WS DOWN-1ESSEE AND POLYPEPTIDES

TITLE OF INVENTION: AND USES THEREPOR

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: BOSCON

COUNTIER READABLE FOOM:

GOUNTHY: US

SOFTWARE: FastESSE OF STANKLIN STREET:

COMPUTER READABLE FOOM:

GOUNTHY: US

SOFTWARE: FastESO VERSION 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/753,007A

CLASSIFICATION UNBER: US/08/753,007A

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/699,591

FILING DATE: 19-AUG-1996

ATTORNEY/AGENT INFORMATION:

APPLICANTION DATA:

APPLICANTON WINBER: 32,983

FREISTRATION WAREER: 32,983

ATTORNEY/AGENT INFORMATION:

RESISTRATION FOR SEQ ID NO: 7:

ELEPHONE: 617-542-8906

ATTORNEY/AGENT INFORMATION:

TELEPHONE: 617-542-8906

ATTORNEY/AGENT INFORMATION:

TELEPHONE: 617-542-8906

TELEPHONE: 617-542-8906

ATTORNEY/AGENT INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 1476 base pairs

FREISTRANDEDEESS: single

TOPICS TYPE: COMMA

FREITH APPLICATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1476 base pairs

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AF146702	PECIT T 1
Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.,	1 (bases 1 to 1034)	Asteridae; lamiids; Solanales; Solanaceae; Petunia.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Petunia x hybrida	Petunia x hybrida		AF146702.1 GI:7673083	cds. AF146702	Petunia x hybrida An2 protein (an2) mRNA, an2-V26 allele, complete	AF146702 1034 bp mRNA linear PLN 01-MAY-2000		

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in the evolution of flower color
Plant Cell 11 (8), 1433-1444 (1999)
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Query Match
Best Local Similarity
Matches 429; Conserv
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 86)
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1087, Amsterdam 1081HV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quattrocchio, F., W. Mol, J. and Koes, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99380006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular analysis of the anthocyanin2 in the evolution of flower color
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Petunia integrifolia
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(bases 1 to 866)
-~hio.F., Wing;J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. and Koes, R.
                                                                                                                                  310
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                                                                                                         COGOLI BURNE CONTROL POR CONTROL PRODUCT CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Petunia
/mol_type="mRNA"
/cultivar="S6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="anz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="petal limb"
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                                                                                                                                                                                                                                                                                                                                                                                                                      note="anthocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="an2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:4103"
chromosome="6"
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                        31.7%;
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  Score 261.6; DB 8
Pred. No. 1.5e-41;
0; Mismatches 174
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Netherlands
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AUTHORS
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   FEATURES
                                 TITLE
JOURNAL
                                                                                                                                    JOURNAL
MEDLINE
                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                       AUTHORS
                                                                                                                      PUBMED
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                                                                                                                                                                                                  Petunia x hybrida
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 868)
Ouattrocchio,F., Wing,J., van der Woude,K., Souer,E.,
Mol,J. and Koes,R.
Submitted (29-APR-1999) Gene
1087, Amsterdam 1081HV, Neth
Location/Qualifiers
                                                                                                                                                  Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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                                                  Direct Submission
                                                                  Quattrocchio, F., W. Mol, J. and Koes, R.
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(bases 1 to 868)
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                                                                                  Woude, K.,
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(an2) mRNA,
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                                                                                   Souer,
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                                                                                   Vetten,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC
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   TTACTGGAAAATTGCAATGACGATATTGAAGAAGATGAAG
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                                  ACTGATGAGAAGCAAAAACCGGAAGATTCGATAGATGGACTTCAATGGTGGGCCAAT
                                                                                                                                    ---ACAAACAATAATGTAATTTTGGACGAGGAGGAACATTGCAAGGAAATAATAA----
                                                                                                                                                                                                     AAACCTCAACGACGCAAGTATTTCTCAAGCACAATGAAGAATGTT-----
                                                                                                                                                                                                                                     CAGAAACAAGAGCAAGAGCTAGCAAAGCCATGAAA--ATCACCGAGAACAACATAATA
                                                                                                                                                                                                                                                                      GTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATTAGTACTAAGATTGAAATTATA
                                                                                                                                                                                                                                                                                                                                                                         CATAAGCTTCTAGGCAACAGATGGTCACTTATAGCTGGAAGACTTCCGGGAAGAACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCTTTTATTGAGAGAATGCATTGACAAGTATGGAGAAAGGGAAAGTGGCATCTAGTTCCA
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                                                                  ----GTGAGAAACAAACTCCAGATGCATCGATGGACAACGTAGATCCATGGTGGATAAAT
                                                                                                     AAAAGTTGTAATAAAAACACTATAGACAAGAATGAAGGTGACACAGAAATAATAAAGTTT
                                                                                                                                                                       AAACCTCGTCCTCGGACCTTCTCAAGGCCGGCAATGAATCATGTTTCTTGTTGGAACGGC
                                                                                                                                                                                                                                                                                                         AACGATGTCAAAAACTATTGGAACACGCACCTTCGAAAGAAGTTAATTGCTCCTCATGAT
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LNRCRKSCRLRWLNYLRPHIKRGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTHLRKKLIAPHDQKQESKS"
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/organism="Petunia x hybrida"
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140 c 19
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/product="An2 truncated protein"
/protein id="AAF66731.1"
/db_xref="GI:7673092"
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/cultivar="W22"
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/chromosome="6"
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Pred. No. 2.2e-41;
0; Mismatches 182;
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JOURNAL
                                                                                                                                                                   Matches
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121
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Submitted (29-APR-1999) Genetics, V.
1087, Amsterdam 1081HV, Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular analysis of the anthocyanin2 gene in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asteridae; lamids; Solanales; Solanaceae;
1 (bases 1 to 868)
Quattrocchio, F., Wing, J., van der Woude, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 868)
Quattrocchio, F., Wi
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                                                     GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC 120
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ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA 180
                                                                                                 ATGAGTACTTCTAATGCATCAACATCAGGAGTAAGGAAAGGTGCATGGACCGAGGAAGAA
                                                                                                                  ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
                                GATCTTTTATTGAGAGAATGCATTGAGAAGTATGGAGAAGGGAAGTGGCATCTAGTTCCG
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                                                                                                                                                                                                                                                    307
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="An2 truncated protein"
/protein_id="AAP66732.1"
/protein_id="AAP66732.1"
/db_xref="G1:7673094"
/translation="MSTSNASTSGVRKGAWTEEEDLLLRECIEKYGEGKWHLVPVRAGLARCKSCRLRWLNYLRPHIKRGDFSLDEVELILRLHKLLGNRWSLIAGRLPGRTAND
                                                                                                                                                                                                                                                 /gene="an2"
/notee="causes frameshift leading
/replace="nnnn"
/ replace="nnnn"
/ 137 c 195 g 229 t
                                                                                                                                                                                                                                                                                                                                    VKNYWNTHLRKKLIAPHDQKQESKS"
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.. .868
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chromosome="6"
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Pred. No. 2.2e-41;
0; Mismatches 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulator;
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                                                                                                                                                                                                                                                                                     truncated
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Petunia integrifolia
Petunia integrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases | 1 to 865)
                                                                                                                                                                                                                                                                                   Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999) 99380006
                                                                                                                                                                   Submitted (29-APR-1999) Genetics, V: 1087, Amsterdam 1081HV, Netherlands
                                                                                                                                                                                                2 (bases 1 to 865)
Quattrocchio, F., Wing, J.,
Mol, J. and Koes, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF146703
Petunia integrifolia
                                                                                                                                                                                                                                                                                                                                                     Mol,J. and Koes,R.
                                                                                                                                                                                                                                                                                                                                                                   Quattrocchio, F.,
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                 /tissue_type="petal limb"
1. .865
/gene="an2"
                                                /db_xref="taxon:4103"
/chromosome="6"
                                                                               /mol_type="mRNA"
/cultivar="S9"
                                                                                                                                                   Location/Qualifiers
                                                                                                                  organism="Petunia integrifolia"
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allele, complete cds. AF146705 AF146705.1 GI:7673089
                                   AF146705 909 bp
Petunia x hybrida An2 truncated
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LNRCRKSCRLRWLNYLRPHKGGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRPAND
VKNYWNTHLRKKLIAPHDQKQESKKAMKITENSIKFRPRTFSRPAMNHVSCWNGKS
CNKNYIDKNEGDTEIIKFGDEKQKPEESIVDGLGWWANLLANNIEIEELVSYNSPTLL
HEETAPSVNAESSLTQEGGSGLSDFSVDIDDIWDLLS"

133 c 193 g 229 t 1 others
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12. .779
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/db_xref="GI:7673086"
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Petunia x hybrida
Petunia x hybrida
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
1 (Dases 1 to 909)
Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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Quattrocchio, F., Wi
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                                                                                                                        GTTAGAGCTGGTCTGAATAGATGCAGGAAAAAGTTGCAGACTTAGGTGGTTGAATTATCTA
                                                                                                                                                      ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA
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                                                                                                                                                                                                                                 GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC
                                                                                                                                                                                                                                                                                                                  ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
  CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCT
                                                                               AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
                                                                                                                                                                                                                                                                                       ATGAGTACTTCTAATGCATCAACATCAGGAGTAAGGAAAGGTGCATGGACCGAGGAAGAA
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/note="causes:
/replace=""
a 137 c 1:
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/protein id="An2 truncated protein"
/protein id="An2 truncated protein"
/db_xref="GI:7673090"
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LNRCRKSCRLEMMLVLRPHIKRGDFSLDEVELILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTHLRKKLIVPHDQKQESKTKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="anthocyanin regulator; myb-related transcription
factor"
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/chromosome="6"
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                                                                                                                                                                                                                                                                                                                       Quattrocchio, F., W Mol, J. and Koes, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamidis; Solanales; Solanaceae; Petunia.

1 (bases 1 to 865)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.
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Petunia axillaris
complete cds.
                                                                                                                                                                                                                                                                                             Submitted (29-APR-1999) Genetics, V 1087, Amsterdam 1081HV, Netherlands
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                                                                                 /gene="an2"
/note="anthocyanin
factor"
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12..374
                                                                                                                                                                                                                                                                                Location/Qualifiers
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'cultivar="S7"
                                                                                                                                                                                                                                                     organism="Petunia axillaris"
                                                                                                                                                                     'tissue_type="petal limb"
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Submitted (29-APR-1999) Genetics,
1087, Amsterdam 1081HV, Netherlan
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamida; Solanales; Solanaceae; Petunia.

1 (bases 1 to 858)
Quattrocchio,F., Wing,J., van der Woude,K., Souer,E., de Vet
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                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-OCT-2001) Shozo Kobayashi, National Institute of Fruit Tree Science, Department of Grape and Persimmon Research; 301-2, Akitsu, Toyota-gun, Hiroshima 729-2494, Japan (E-mail:skobaya@affrc.go.jp, Tel:81-846-45-4719,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kobayashi,S., Ishimaru,M., Hira
Myb-related genes of the Kyoho
anthocyanin biosynthesis
Planta_215 (6), 924-933 (2002)
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/note="anthocyanin regulator"
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                                                                                                                                                                                                                                                                                    cultivar="Kyoho"
                                                                                                                                                                                                                                                                                                                     organism="Vitis labrusca
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                                                                                                                                          Direct Submission
Submitted (15-OCT-2001) Shozo Kobayashi, National Institute of Fruit Tree Science, Department of Grape and Persimmon Research; 301-2, Akitsu, Toyota-gun, Hiroshima 729-2494, Japan [B-mail:skobaya@affrc.go.jp, Tel:81-846-45-4719,
                                                                                                                                                                                                                                                                      Kobayashi,S., Ishimaru,M., Hira
Myb-related genes of the Kyoho
anthocyanin biosynthesis
Planta 215 (6), 924-933 (2002)
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1. .1173
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Vitis labrusca x Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core er
rosids; Vitaceae; Vitis.
Direct Submission
Submitted (15-OCT-2001) Shozo Kobayashi, National Institute
Fruit Tree Science, Department of Grape and Persimmon Reseas
301-2, Akitsu, Toyota-gun, Hiroshima 729-2494, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB073012 903 bp
Vitis labrusca x Vitis vinifera
transcription factor VlMYBA1-2,
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Myb-related genes of the Kyoho
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Planta 215 (6), 924-933 (2002)
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/note="anthocyanin regulator"
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10. .933
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                                                                                                            903)
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Pred. No. 1.6e-29;
0; Mismatches 81
                                                                                                                                                                                                                  Hiraoka,K.
(yoho grape (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA linear PLN 21-NOV
VlmybA1-2 gene for myb-related
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                                                                                                                                                                                                                                                                                                            a; Tracheophyta;
eudicots;
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Matches
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 420)
Stracke,R., Werber,M. and Weisshaar,B.
                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                    complete cds.
AY008379
                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                     AY008379
                                                 Spermatophyta; Magnoliophyta; eudicotyledons;
                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                   AY008379.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (E-mail:skobaya@affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                               CTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGGATTATCTAAGGCCACATATC
                                                                                                                                                                                                                                                                                        AACTATTGGCATGGTCACCACTTGAAAAAG
                                                                                                                                                                                                                                                                                                                       AACTATTGGAACACTAATCTTCTAAGGAAG
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SSKPSSTSPQFNDDIIWESLLAELDQETDFSASGEMLIASLRAEETATQKKGPNDGM
IEQIQQEEGDFPFDVGFMDTPNTQVNHLI"
1 168 c 205 g 222 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MESLGVRKGAWIQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCR
KSCRLRWLNYLKPDIKRGEFALDEVDLMIRLHNLLGNRWSLIAGRLPGRTANDVKNYW
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/protein_id="BAC07539.1"
/db_xref="GI:22266665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="activate the Kyoho
/note="anthocyanin regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "mol_type="mRNA"
'cultivar="Kyoho"
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Pred. No. 1.4e-28;
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s transcription factor MYB114 mRNA,
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JOURNAL
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TITLE
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                                                                                                                                                                    992 bp
Arabidopsis thaliana production
(PAP2) mRNA, complete cds.
Borevitz,J.O., Xia,Y., Blount,J., Dixon,R.A. and Lamb,C. Activation tagging identifies a conserved MYB regulator
                1 (bases 1 to 992)
Borevitz, J.O., Xia, Y.,
                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-SEP-2000) Dept. Biochemie, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 420)
Stracke, R. and Weisshaar, B.
                                                                                                              Arabidopsis thaliana (thale cress)
                                                                                                                                                AF325124.1
                                                                                                                                                                 AF325124
                                                  rosids;
                                                                                                                                                                                                                                                                                                                           TGGAACACTAATCTTCTAAGGAAG
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                                                                                                                                                                                                                                                                                             TGGAACACCCATCTGAGTAAGAAG
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                                                  eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEGSSKCLRKGAWTAEEDSLLRQCIGKYGEGKWHQYPLRAGINR
CRKSCRLRWLNYLKPSIKRGKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKN
YWNTHLSKKHEPCCKTKIKRINIITPPNTPAQKVDIF"
67 c 105 g 114 t
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/db_xref="GI:11641124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="1"
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                                                                                                                                                GI:11935172
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                                                II; Brassicales; Brassicaceae;
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Pred. No. 2.5e-:
0; Mismatches
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Sequence 3 from
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Arabidopsis thaliana (thale cress)
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153 c 221 g 310 t
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CRKSCRLRWLNYLKPSIKRGRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKN
YWNTHLSKKHESSCCKSKMKKKNIISPPTTPVQKIGVFKPRPRSFSVNNGCSHLNGLP
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/protein_id="AAG42002.1"
/db_xref="GI:11935173"
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/chromosome="1"
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cultivar="Columbia-0"
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            2 (bases 1 to 1033)
Greco,R., Petroni,K.
Direct Submission
                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1033)

1 (bases 1 to 1033)

1 (Branz, H.D., Denekamp, M., Greco, R., Jin, H., Leyva, A., Meissner, R.C., Petroni, K., Urzainqui, A., Bevan, M., Martin, C., Smeekens, S., Tonelli, C., Paz-Ares, J. and Weisshaar, B.
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                                                                                                                                                Towards functional characterisation of the members gene family from Arabidopsis thaliana plant J. 16 (2), 263-276 (1998)
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(MYB90) mRNA,
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Search completed: January 30, 2004, 07:56:37 Job time : 2218 secs
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Best Local Similarity 74.5%;
Matches 234; Conservative
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                                                                                                                                                                               362 AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC 421
                                                                                                                                                                                                                  259 AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT 318
                                                                                                                                                                                                                                                                        302 GGAAGACTTAGCAATGATGAAGTTGATCTTCTTCGCCTTCATAAGCTTCTAGGAAAT
                                                                                                                                                                                                                                                                                                                     199 GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                                                                                                                                                                                                                                                                                                 242 CGATGCAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 TGTATTGATAAGTATGGAGAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEGSSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNR CRKSCRLRWLNYLKPSIKGRLSNDEVDLLLRLHKLLGNRWELLHGRLPGRTANDYKN YMNTHLSKKHESSCCKSKMKKKNIISPTTVVQKIGVFKPRPRSFSVNNGCSHLNGLPEVDLIBSCLGLKKUNVCENSITCNKDEKDDFVNNLMNGDNMHLENLLGENQEADAIV PEATTAEHGATLAFDVEQLWSLFDGETVELD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MYB90; R2R3-MYB factor family member"
/codon_start=1
/product="putative transcription factor"
/protein_id="AAC83637.1"
/db_xref="GI-3941522"
/db_xref="GI-3941522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Columbia"
/db_xref="taxon:3702"
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Maximum Match 100%
Listing first 45 summaries
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                                                                     825
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Tomato anthocyanin
Tomato anthocyanin
Arabidopsis thalia
Arabidopsis cDNA e
Arabidopsis thalia
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Arabidopsis thalia
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Arabidopsis thalia	AAC33633	21	1203	16.3	134.6	45	
	ABL93882	24	452	16.4	•	44	
	ABT08114	24	1236	•	135.8	43	
	AAD06651	22	1082		136.2	42	
	AAC47037	21	1392	16.7	138	41	
Arabidopsis thalia	AAC49321	21	1329		138	40	
œ	AAF84746	22	1310		138	39	
	AAC50981	21	1280	•	138	ა 8	
Arabidopsis thalia	ABZ14333	24	960	•	138	37	
യ	AAC57227	21	373		138	36	
00	ABK65183	24	660	16.8	138.6	3 5	
Arabidopsis thalia	AAC40461	21	1332		139.6	34	
	AAD06466	22	918	17.3	143	ω u	
	AAC42479	21	839	•	143	32	
	ABZ14541	24	810		143	31	
o	ABK65317	24	612	•	143.4	30	
Cotton transcripti	AAF90596	22	1081	17.4	143.8	29	
Cotton transcripti	AAF90594	22	1006	17.4	143.8	28	
Cotton transcripti	AAF90595	22	1151	17.5	144.4	27	
	AAC51202	21	639		146.8	26	
	AAC34284	21	871	17.8	147	25	
	AAC49989	21	868	17.8	147	24	
Arabidopsis thalia	ABN99077	24	791	17.8	147		ი
	AAF80412	22	764	17.8	147	22	
Nucleotide sequenc	AAF85190	22	933	18.5	153	21	
rt	AAC56371	21	504	18.6	153.2	20	
	ABZ14831	24	774	18.8	154.8	19	
	AAC42662	21	774	18.8	154.8	18	
Myb-related transc	ABT08113	24	514	19.1	157.4	17	
ā	ABX20395	25	390	•	170.6	16	
	ABK65341	24	925	•	179	15	
Arabidopsis thalia	ABZ14829	24	747	•	179	14	
	ABK14221	24	956	•	180.2	13	
	ABK65363	24	741	•	185.4	12	
ΩO.	AAD05767	22	741	22.5	185.4	11	
Ω0	AAF85191	22	1043	•	œ	10	
Arabidopsis thalia	AAD47497	25	1033	•	186	9	

ALIGNMENTS

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RRESULT 1
AB073046
ID AB077
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Conners K, Mathews HV, Liu A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomato anthocyanin 1 (ANT1) encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200255658-A2.
                                                                                                        (EXEL-) EXELIXIS PLANT SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "anthocyanin mutant (ANT1)"
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Query Match
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Matches 825
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes tomato anthocyanin 1 (ANT1). The ANT1 polynucleotide can be used for modifying the expression of a native plant gene, particularly for producing an anthocyanin 1 phenotype in plants, which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 39; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colour or fruit colour in plants.
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DB; ABB81626.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
CATGAAAATTGGGGTGAATTTTCTCTTAATTTACCACCCATGCAACAAGGAGTACAAAAT
                                                                            GAAATATCACCACCATTAAATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGT
                                                                                                                                                 GAAGAAGATGAAGATGTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
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                                                       GAAATATCACCACCATTAAATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGT
                                                                                                                              GAAGAAGATGAAGAGGTTGTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
                                                                                                                                                                                                                          TCGATGGACAACGTAGATCCATGGTGGATAAATTTACTGGAAAATTGCAATGACGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCT
                                                                                                                                                                                                   TCGATGGACAACGTAGATCCATGGTGGATAAATTTACTGGAAAATTTGCAATGACGATATT
                                                                                                                                                                                                                                                                            GTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATTAGTACTAAGATTGAAATTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes tomato anthocyanin 1 (ANT1). The ANT1 polynucleotide can be used for modifying the expression of a native plant gene, particularly for producing an anthocyanin 1 phenotype in plants, which is responsible for many red and blue colours in plants. The present sequence represents an anticular of the polynucleotide is useful for modifying e.g. leaf colour, flower colour or fruit colour in plants. The present sequence represents an ANT1 genomic DNA fragment which is used in an example from the present and the present sequence represents the present seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAATTGTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATTAGTACTAAGATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACAGCTAACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGGAAGTTAAATACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGGCAT
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                                                                                                                                                                                     biotechnology;
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                           Location/Qualifiers
product= "Transcription factor homologue G2421"
                                                                                                                                                                                                                                                                                            transcription factor homologue G2421 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             762
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                                                                                                                                                                                                           therapy;
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                                                                                                                                                                                                                                                                                                                                         The present cDNA sequence is homologue G2421 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination transcription factor levels in plants offers great potential in garicultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                        Sequence 762 BP; 225 A; 109 C; 193 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 115; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reuber
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(PILG/)
(RIEC/)
(JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-1999; 99US-0166228
17-APR-2000; 2000US-0197899
22-AUG-2000; 2000US-0227439
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DB; AAE01933.
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PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIECHMANN J L.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREELMAN R.
                                                                                                                         AGATGTCGGAAAAGTTGTAGATTGAGGTCGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                                                                                                                                          TGTATTGATĀAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATĀAGAGCTGGTCTGAAT
                                                                                                                                                                                                                                        TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA
AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT
                                                                                               CGGTGCAGGAAAAGTTGTAGACTAAGATGGTTAAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                    TCGTCCAAAGGGTTGAAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCAG
                                     GGAAĀATTTAGTTCTGĀTGĀĀGTTGĀTCTTCTTCTTCGTCTTCĀTĀĀGCTTCTĀGGAĀĀT
                                                                   GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Creelman
Heard J;
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                          23.0%;
74.1%;
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                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                          Score 189.6; DB Pred. No. 6.5e-37
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z,
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                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                          Length
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AGGTGGTCCTTGATTGCTGGTCGATTACCTGGTCGGACCGCTAATGATGTCAAGAACTAC

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RESULT 4
ABK65362
AD ABK6
XX ABK6
XX ABK6
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XX ABK6
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DT 02-J
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KW Plan
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KW Frui
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PR 16-1

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                            encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a plant ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; ss; gene; (agriculture; metal microbial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis cDNA encoding a transcription factor #214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated or recombinant polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DUBE/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEND-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REUB/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JIAN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PINE/)
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DB; AAU93176.
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ADAM L.

/) RATCLIFF O.

TEUBER J L.

TANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREELMAN R.
DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 877-878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAACACTAATCTTCTAAGGAAG
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sease resistance; herbicide resistance; seed yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R, Dubell AJ, Heard C
Reuber JL, Riechmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  941pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            produce a transgenic
          polynucleotide that
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Pineda O;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A. thaliana transcription factor.
ABN98500 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 762 BP; 225 A; 109 C; 193 G; 235 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                       AGATGTCGGAAAAGTTGTAGATTGAGGTTGGCTGAATTATCTAAGGCCCACATATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                             TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT
                                                                                         TGGAACACCCATCTGAGTAAGAAG 333
                                                                                                                           TGGAACACTAATCTTCTAAGGAAG 342
                                                                                                                                                                                        AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
                                                                                                                                                                                                                                                            GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
                                                                                                                                                                                                                                                                                                              CGGTGCAGGAAAAGTTGTAGACTAAGATGGTTAAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                      TGTATTGGTAAGTATGGAGAAGGCAAATGGCATCAAGTTCCTTTAAGAGCTGGGCTAAAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCAG
                                                                                                                                                               AGGTGGTCCTTGATTGCTGGTCGATTACCTGGTCGGACCGCTAATGATGTCAAGAACTAC
                                                                                                                                                                                                                                      GGAAAATTTAGTTCTGATGAAGTTGATCTTCTTCTTCGTCTTCATAAGCTTCTAGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.0%;
 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 189.6; DB 2
Pred. No. 6.5e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Length 762;
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RESULT 5
ABN98500/c
ID ABN985
XX ABN985
XX O1-AUG
DT O1-AUG
XX Arabid
XX Arabid
XX Arabid
XX Arabid
XX INTIT
OS Arabid
XX US2002
XX US2002
XX US2002
XX 21-FEB
XX 27-JAN
XX 27-JAN
XX (GORL/
PA (RANY/)
PA (RANN/)
                 (HAMI/)
(PRIC/)
(RAIN/)
                                                                                                                                     26-JAN-2001; 2001US-0770445.
                                                                                                                                                                    21-FEB-2002
                                                                                                                                                                                                 US2002023281-A1
                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                       Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; disease; crop; thale cress; tolerance factor; insect; pathogen;
                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana expressed polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                 01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                              ABN98500;
                                                             (GORL/)
(ANYY/)
                                                                                                       27-JAN-2000; 2000US-178472P
 PRICE J L.
RAINES T M.
YU Y.
                                                                          GORLACH J.
                                                             AN Y.
                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                               entry)
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IJ

g 268

(RAME/)

MATHEW A V. RAMEAKA J G

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                                                                                                                                                                                                                                                                                                                      The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions CC comprising a sequence selected from any one of 99 sequences (ABN98231-ABN99231), CC given in the specification or its fragment. A polypeptide (II) encoded by (I), a transgenic plant (III) comprising an exogenous nucleic acid or a CC genetically modified cell (IV) comprising an exogenous nucleic acid, is CC useful in identifying homologous or related genes, in producing CC compositions that modulate the expression or function of its encoded CC protein, mapping functional regions of the protein and in studying a saociated physiological pathways. (I) is also useful for the genetic CC manipulation of cells, particularly plant cells. (I) is also useful in CC screening assays of various plant strains to determine the strains that CC are best capable of withstanding a particular disease or environmental CC stress. (II) and (III) are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc., for elucidating biochemical cc pathways. The screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening CC programs to identify agents that mimic or enhance the action of tolerance for enhance their tolerance to environmental stress. (I) is also useful for comparance to inhibiting production of a biosynthetic product in a CC expression of proteins of interest, for establishing the extent to which capacitic insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress, for identifying factors involved in biosynthetic productions of nutritional, commercial or medicinal value and cc particular plant, for of of the protein of the expression of puritional, commercial or medicinal value and concerning or inductions of nutritional.
                                                                             Matches
                                                                                           Query Match
Best Local 9
                                                                                                                                                                                       for identifying productions of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products. Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from USP at seqdata.uspto.gov/sequence.html?DocID=999909770445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garcia
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(LEDF/)
(WOES/)
                                                                                                                                                      Sequence 982 BP; 303 A; 215 C; 140 G; 322 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded protein, and mapping functional regions of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-400781/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KRIC/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; SEQ ID
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DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                             Similarity
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GARCIA C A.
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                                      TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
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, Page A, M
Kricker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO 268; 49pp + Sequence Listing; English
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                                                                                             22.5%;
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                                                                                             Score 186; DB 24;
Pred. No. 5.3e-36;
                                                                           Mismatches
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Ledford BL,
, Davis KR,
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Hoffman N;
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RESULT
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17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription factor; trait modification; seed characteristic; structural characteristic; developmental characteristic; gene agricultural biotechnology; ss.
                          vocleic acids encoding plant transcription factor polypeptides, useful for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                               Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana transcription factor G663 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD05751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD05751 standard; cDNA; 1033
                                                                   P-PSDB; AAE01916
                                                                             WPI; 2001-335979/35.
                                                                                                  Pineda
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                                                                                                                                                                                           (PILG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                                                                  Ó L
                                                                                                                                             YU G.
PINEDA O.
                                                                                                                                                                 RIECHMANN J L.
JIANG C.
                                                                                                                                    HEARD J.
                                                                                                                                                                                           PILGRIM M.
                                                                                                                                                                                                                          MENDEL
                                                                                                                                                                                                    CREELMAN R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAGACTTAGCAATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAAAT
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                                                                                                  Heard
                                                                                                              Creelman
                                                                                                                                                                                                                                               ; 99US-0166228.
; 2000US-0197899.
; 2000US-0227439.
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                                                                                                                                                                                                                          BIOTECHNOLOGY INC
                                                                                                  J;
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                             Pilgrim M,
                                                                                                              Riechmann JL,
                                                                                                              Jiang
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Claim 4; Page 69-70; 133pp; English plants, e.g. corn, potato and

cotton plants

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RESULT 7
ABK65155
ID ABK6
XX ABK6
DT 02-,
DT 02-,
XX P1
BX ATA
AX P1
KW P1
KW P1
KW Er
XX
OS Ar
XX
PN WC
XX
PD 21
FX
PF 2
PF 2
PF 2
PR 1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is Arabidopsis thaliana transcription factor 666 cDNA. The transcription factors may be used to modify traits associate with structural or developmental characteristics of plants, cor potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, to modify vitamin and mineral content, to modif the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phrenyl lipid content, to modify fatty acid and modifications.
 22-AUG-2000;
16-NOV-2000;
16-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a
                                                                                                                                                                                                          plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1033 BP;
                                                                      22-AUG-2001;
                                                                                                                                           WO200215675-A1
                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                Arabidopsis cDNA encoding a transcription factor #7.
                                                                                                                                                                                                                                                                                                                                      02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                        ABK65155;
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Similarity 74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAACACTAATCT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCCACATATCAAGAGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTATTGATAAGTATGGAGAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAACACCCATCT 435
 ; 2000US-227439P.
; 2000US-0713994.
; 2001US-0837944.
                                                                      2001WO-US26189.
                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 186; DB 22;
Pred. No. 5.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; 226 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                          В₽
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258 301 198 241

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CGATGCAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA TGTATTGATAAGTATGGAGAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAAT

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                                                                                                                                                                                                                                                                                        cc associated with a plant trait as compared to a wild plant. Also included care a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a commologue sequence from a database comprising a plurality of known plant sequences comprising a plurality of known plant computers of the first polynucleotide is used for producing a plant having a composition of the isolated or recombinant polynucleotide is used for producing a plant having a condified trait, the method comprising selecting a polynucleotide that composition of a plant having a condisting the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, inserting the conficting for antisense nucleic acid, thereby producing a modified confiction of agriculturally useful proteins or metabolic chemicals, pest tolerance, herbicide resistance, seed and fruit yield, growth conficient proteins or resistance, seed and fruit yield, growth conficient proteins or series in the first plant of the conficience of the polyperiod conficiency herbicide resistance, seed and fruit yield, growth conficiency and selecting for a cell of a plant to protein the conficiency herbicide resistance, seed and fruit yield, growth conficiency and selecting for a cell of the proteins or metabolic chemicals.
                                                                                                                            Query Match
Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant path the plant or the plant or the plant exhibits as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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(PILG/)
(CREE/)
(CREE/)
(DUBE/)
(HEAR/)
(JIAN/)
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                      specification). encoding an A. t
                                                                                                                                                                                                                                                                                rate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated or recombinant polynucleotide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pilgrim
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(ADAM/)
(RATC/)
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                                                     122
                                                                                                                                                                                                                                        leaf and flower senescence and many other traits listed fication). The present sequence is one of the 232 polynucing an A. thaliana transcription factor.
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JIANG C.
KEDDIE J.
ADAM L.
RATCLIFF O.
REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YU G.
PINEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MENDEL BIOTECHNOLOGY INC. PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REUBER J L.
RIECHMANN J
                                                                                                                                                                                                       1033
TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT
                                                     TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCTA
                                                                                          TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95-96; 941pp; English
                                                                                                                                                                                                     BP; 334 A; 161 C; 226 G; 312 T; 0 other;
                                                                                                                                              22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R, Dubell AJ, Heard J, Reuber JL, Riechmann JL,
                                                                                                                              0;
                                                                                                                              Score 186; DB Pred. No. 5.4e 0; Mismatches
                                                                                                                                                                   DB 24;
                                                                                                                                                  .4e-36
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                                                                                                                                                                 Length 1033;
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                                                                                                                                Indels
                                                                                                                                                                                                                                                             polynucleotides
                                                                                                                                                                                                                                                                           yht,
yield, g.
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ABKILT 8
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               This invention relates to the nucleotide and protein sequences of novel Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromosomus 1. PAP1 and PAP2 are WYB-like transcription factors that regulate the production of anthocyanin pigment. The nucleotide sequence of the invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for plant cell (e.g., A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour
                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAP2; production of anthocyanin pigment; MYB-like transcription factor; transgenic; plant; phenylpropanoid; stress; light stress; water stress; pH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK14222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borevitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. thaliana Production of anthocyanin pigment 2 (PAP2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SALK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-164443/21.
DB; AAU75735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBERTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "PAP2
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  (pos:593..595, aa:Xaa)
  (pos:680..682, aa:Xaa)
  (pos:755..757, aa:Xaa)
  (pos:842..844, aa:Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dixon RA;
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                                                                                                                                                                                                                                                                                                                                                                                                          alkaloid pathway gene; taxadiene synthase; biological pathway; free: abiotic stress; cold; drought; heat; nutrient deficiency; biotic stinfection; developmental pathway; flowering; root development; TDS; transgenic; transgenic plant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1033 BP; 334 A; 161 C;
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                                                                                                                     WO200274917-A2
                                                                                                                                                                                                                                                                                                                                                        Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription factor; metabolite pathway; terpenoid; limonene synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana G663 transcription factor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD47497 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319
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/product= "Arabidopsis thaliana G663
/product= "Arabidopsis thaliana G663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         freezing;
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15-MAR-2002; 2002WO-US07999.

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a polynucleotide which encodes a transcription factor for controlling the expression of one or more genes in a pathway. The method is useful for determining whether a member of a pool of test transcription factor or polynucleotides encodes a biosynthetic pathway transcription factor or a primary metabolite pathway gene or a secondary metabolite pathway gene a primary metabolite pathway to be pathway gene or a perimary metabolite pathway gene transcription factor. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flowering, root development, a response pathway to environmental cues such as light intensity and light quality, circadian rhythm. Sequences of the invention are used to generate transgenic plants. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining whether one of several test transcription factor (TF) polynucleotides encodes pathway TF by determining expression from pathway gene promoter linked to reporter gene in a cell in presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1033 BP; 334 A; 161 C; 226 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 153; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE30046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is Arabidopsis thaliana G663 transcription factor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEND-) MENDEL BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                       AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCTA
                                                                                                  TGGAACACCCATCT
                                                                                                                                      TGGAACACTAATCT 332
                                                                                                                                                                                                                      AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
                                                                                                                                                                                                                                                                                                 GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA
                                                                                                                                                                               AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC
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74.5%;
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                                                                                                    435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 186; DB 25;
Pred. No. 5.4e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB60 MYB polypeptides are useful for enhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, flavonoids, lignins, salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resistance a crop in a field -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cbs
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1043 BP; 334 A; 166 C;
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23-OCT-2000; 2000US-0693855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of MYB transcription factor AtMYB90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF85191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BADI ) BASF
                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-316365/33.
                        302
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                                                                                                                                        139
                                                                                                                                                                                 182
                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Fig 4; 92pp;
                                                                                                                                                                                                                                                                                                      19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCCTTAAGAAAA
                                                                                                                                                                                                                                                                                                                                        234;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                    AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                       GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
                                                                                                                                                                               TGTATTGATAAGTATGGAGAAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAAT
                                                                                                                                                                                                                      TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCCATAAGAGCTGGTCTGAAT
                                                                                                                                                                                                                                                             TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCTA
                        GGAAGACTTAGCAATGATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAAT
                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product=
                                                                                                                                                                                                                                                                                                                                                           22.5%;
74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "MYB transcription
                                                                                                      AGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                           Score 186; DB 22;
Pred. No. 5.4e-36;
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Mismatches

80;

0,

Gaps

181

78

361

301 198 241 138

Length 1043; Indels

231 G;

312 T; 0 other;

for

of.

AAF85191 standard; cDNA; 1043 BP

78 147

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RESULT 11
AAD05767
ID AAD05
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The present cDNA sequence is homologue G2422 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the insoluble sugar content of seeds, to modify the plants acid and modify wax content. They may alipid content, to modify fatty acid and modify wax content. They may alipid content seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination
                                                                                                                                                                              Nucleic acids encoding plant transcription factor polypeptides, to for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription factor; trait modification; seed characteristic; structural characteristic; developmental characteristic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001
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                                                                                                                                                                                                                                                                                     Reuber
                                                                                                                                                                                                                                                                                                                                                                                                   (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-2000; 2000WO-US31457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200135727-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD05767 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                    (YUGG/
                                                                                                                                                                                                                                                                                                                                                   (JIAN/
                                                                                                                                                                                                                                                                                                                                                               (RIEC,
                                                                                                                                                                                                                                                                                                                                                                           (PILG/
                                                                                                                                                                                                                                                                                                                                                                                        (CREE/)
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                                                                                                                                                       4; Page 113; 133pp;
                                                                                                                                                                                                                                                                      Ó.L
                                                                                                                                                                                                                                                                                                           PILGRIM M.

RIECHMANN J L.

JIANG C.

YU G.

PINEDA O.

HEARD J.
                                                                                                                                                                                                                                     AAE01932.
                                                                                                                                                                                                                                                                                                                                                                                                                 MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                       CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                    REUBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGAACACCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAACACTAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
                                                                                                                                                                                                                                                                      Creelman
Heard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0166228.
2000US-0197899.
2000US-0227439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biotechnology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "Transcription factor homologue G2422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                               ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription factor homologue G2422
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                                                                                                                                                                                                                                                                                   Pilgrim
                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                     Z,
                                                                                                                                                                                                                                                                                     Riechmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characteristic; gene therapy;
                                                                                                                                                                                                                                                                                   ĮĮ,
                                                                                                                                                                                                                                                                                   Jiang
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                                                                                                                                                                                                         useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                               22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                                                                                                                                                                                                                                                                                             Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                       (DUBE/)
                                                                                                (PILG/)
                                                                                                                                                                                                22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                 WO200215675-A1.
                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis cDNA encoding a transcription
                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK65363 standard; cDNA; 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 741 BP; 237 A; 122 C; 174 G; 208 T; 0 other;
            (RATC/)
                                     (KEDD/)
(ADAM/)
                                                             (JIAN/)
                                                                                                                          (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234;
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RATCLIFF O.
REUBER J L.
RIECHMANN J L.
                                            HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                 CREELMAN
                                                                                      DUBELL
                                                                                                                        MENDEL BIOTECHNOLOGY
                                     ADAM L.
                                                                                                             PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGTGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTTGAGTAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCTTCTAAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGATCGCTGGTAGATTGCCTGGTCGGACTGCTAATGATGTCAAGAATTACTGGAACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTATGGAGAAGGCAAATGGCATCGAGTTCCTTTAAGAACTGGTCTCAATCGGTGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTTGAGAAAAGGTACATGGACTACTGAAGAAGATATTCTCTTGAGGCAATGCATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTCCGATGAAGTTGATCTTGTTCTTCGCCTTCATAAACTTCTAGGAAATAGGTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAGTTGTAGACTTAGATGGTTGAATTATTTGAAGCCAAGTATTAAGAGAGGAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                AN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 185.4; DB 2
Pred. No. 6.9e-36;
                                                                                                                                                                                                                                                                                                                                                          factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC as sociated with a plant trait as compared to a wild-type or reference plant, or the plant comprised to a wild-type or more genes CC associated with a plant trait as compared to a wild plant, or the plant CC trait as compared to a wild plant, or the plant CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising a plurality of known plant CC sequences comprising sequence information selected from one of CC 464 fully defined sequences given in the specification. The isolated or CC encodes a polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a polynucleotide that CC polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexyress CC introducing the vector into a plant or a cell of a plant to overexyress CC plant, and selecting for a modified trait (e.g. increased chemicals, pest tolerance, environmental stress response (e.g. drought), microbial CC disease resistance, herbicide resistance, seed and fruit yield, growth CC rate, leaf and flower sensescence and many other traits listed in the CC encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-292022/33.
P-PSDB; AAU93177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 741 BP; 237 A; 122 C; 174 G; 208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YUGG/) YU G.
(PINE/) PINEDA O.
319
                                                                                                                                                                                                                                                                                      148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Page 879-880; 941pp; English
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Ratcliff O,
CATTTGAGTAAGAAG
                                                                                                                                                               TGCTCCGATGAAGTTGATCTTGTTCTTCGCCTTCATAAACTTCTAGGAAATAGGTGGTCC
                                                                                                                                                                                                                                                                                      AAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGGGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT
                                    AATCTTCTAAGGAAG 342
                                                                              TTGATCGCTGGTAGATTGCCTGGTCGGACTGCTAATGATGTCAAGAATTACTGGAACACT
                                                                                                                  CTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACT
                                                                                                                                                                                                   GAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA
                                                                                                                                                                                                                                                AAGAGTTGTAGACTTAGATGGTTGAATTATTTGAAGCCAAGTATTAAGAGAGGAAAACTC
                                                                                                                                                                                                                                                                                                                                                                       AAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATGTCGG 147
                                                                                                                                                                                                                                                                                                                                                                                                             GGGTTGAGAAAAGGTACATGGACTACTGAAGAAGATATTCTCTTGAGGCAATGCATTGAT
                                                                                                                                                                                                                                                                                                                              AAGTATGGAGAAGGCAAATGGCATCGAGTTCCTTTAAGAACTGGTCTCAATCGGTGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R, Dubell AJ, Heard J
Reuber JL, Riechmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 185.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 6.9e-36;
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האיים JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Indels
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L, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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Pineda O;
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RESULT 13

Query Match Best Local Similarity

21.8%; 68.0%;

Score 180.2; DB 2 Pred. No. 1.4e-34;

DB 24; Length 956;

Sequence

956 B₽;

310 A; 162 C; 202 G; 282 T; 0 other;

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CR Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 CC Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 CC or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromosome C1. PAP1 and PAP2 are MYB-like transcription factors that regulate the CC invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The CC useful for detecting promoter activity within a plant cell (e.g., A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour expression. The nucleotide sequence is also useful for enhancing accumulation of phenylpropanoid product in a plant. A transgenic CC plant is useful for detecting a stress condition such as light tress, water stress, pH stress, temperature stress, heavy metal CC stress, water stress, pH stress, temperature stress, heavy metal CC stress, pathogen attack or infection, wounding, nutrient deficiency, CC clouration in ornamental plants for commercial sales, and for colouration plants to stress. Introduction of PAP1 or PAP2 sensitises CC plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental CC sentence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic; plant; phenylpropanoid; stress; light stress; water stress; pH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borevitz J, Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. thaliana Production of anthocyanin pigment 1 (PAP1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK14221 standard; cDNA; 956 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SALK ) SALK INST BIOLOGICAL STUDIES (ROBE-) ROBERTS NOBLE FOUND INC SAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production of anthocyanin pigment; MYB-like transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sensitisation; gene; ss; chromosome 1.
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                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=  a
/product= "PAP1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73..819
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          cell has been exposed, comprising:
(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant
                                                                                                                                                                                                                     24-AUG-2000; 2000US-227866P.
26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
                                                                                                    Identifying a stress and producing plants
                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana; plant;
                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ14829 standard; DNA; 747
                                          The invention relates to identifying a stress
                                                                    Claim 144;
                                                                                                                                                             Harper JF,
                                                                                                                                                                                                                                                                  24-AUG-2001; 2001WO-US26685
                                                                                                                                                                                                                                                                                          28-FEB-2002
                                                                                                                                                                                                                                                                                                                WO200216655-A2
genome; and
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SYNGENTA PARTICIPATIONS
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                                                                  SEQ ID NO 2634; 577pp + Sequence Listing;
                                                                                                                                                             Kreps J,
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                    condition to which a plant cell has been exposed with increased tolerance to these abiotic stress
                                                                                                                                                                                                                                                                                                                                                                                   stress
                                                                                                                                                             Wang X,
                                                                                                                                                                                                                                                                                                                                                                                 regulated
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                                                                                                                                                             Zhu
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XX Plant
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XX Plant
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Best Local S
Matches 233
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Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; microbial disease resistance; see fruit yield; growth rate; leaf senescence; flower senes
                                                                                                                                                                            22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                                             (MEND-)
(PILG/)
(CREE/)
(DUBE/)
                                                                                                                                                                                                                                                                                  22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                         WO200215675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis cDNA encoding a transcription factor #193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK65341;
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DUBELL A J.
) HEARD J.
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233; Conserv
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                                                                                                      PILGRIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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72.1%;
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0; Mismatches
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.6e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated with a plant trait as compared to a wild plant. Also included associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a chomologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information. The isolated or sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense mucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, most of agriculturally useful proteins or metabolic chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rate, lear and resent sequence - specification. The present sequence - encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes exhibits ectopic expression or altered expression of one or more genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pilgrim M, Creelman
Adam L, Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pest tolerance, environmental stress response (e.g. drought), microbia disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 925 BP; 290 A; 160 C; 200 G; 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 792-794; 941pp; English
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(RATC/)
(REUB/)
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) KEDDIE J.
) ADAM L.
) RATCLIFF O.
REUBER J L.
) RIECHMANN J L.
) YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                         AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT 318
                                                                                                                                                                                                          АGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCCACATATCAAGAGA 198
                                                                                                                                                                                                                                                                             TGTATTGATAAGTATGGTGAAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 138
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                                                                                                                           GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                                                                                                     CGGTGCAGGAAAAGTTGTAGATTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                                                                                        TCGTCCAAAGGGCTGCGAAAAGGTGCTTGGACTACTGAAGAAGATAGTCTCTTGAGACAG 127
                                                                                                                                                                                                                                                     TGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAAC 187
  AGGTGGTCTTTAATTGCTGGAAGATTACCTGGTCGGACCGCAAATGACGTCAAGAATTAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 179; DB 24; Length Pred. No. 2.7e-34; O; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        90; Indels
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L, Yu G,
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Pineda O;
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Search completed: January 30, 2004, 07:19:18 Job time: 243 secs

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Result
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Listing first 45 summaries
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Maximum DB
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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126.6
85.2
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1: /cgn2_6/ptodata/2.
2: /cgn2_6/ptodata/2.
3: /cgn2_6/ptodata/2.
4: /cgn2_6/ptodata/2.
5: /cgn2_6/ptodata/2.
6: /cgn2_6/ptodata/2.
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Match
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Gapop 10.0 , Gapext 1.0
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825
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                           atgaacagtacatctatgtc.....tatggaatctacttgattaa 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
/cgn2 6/ptodata/2/ina/5B_COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/BTTUS_COMB.seq:*
/cgn2 6/ptodata/2/ina/backfiles1.seq:*
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
       4 US-09-610-185C-3
4 US-09-610-185C-1
2 US-09-608-722-628-1
3 US-09-008-979A-2
3 US-09-460-618-2
4 US-09-402-929-1
4 US-09-402-929-1
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8 US-09-10-2358-6
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8 US-09-10-2358-6
8 US-09-132-10
9 US-09-133-14
9 US-09-133-15
9 US-08-3651-90
9 US-08-3651-91
9 US-08-465-139-1
9 US-08-465-139-5
9 US-08-366-6918-46
9 US-08-750-357-1
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Sequence 46, Appli
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Qy 319 TGGAACACTAATCT	Qy 259 AGATGGTCAC Db 362 AGGTGGTCCT	OY 199 GGTGACTTTO	Oy 139 AGATGTCGGI Db 242 CGATGCAGAI	Qy 79 TGTATTGATJ Db 182 TGTATTGATJ	Qy 19 TCTTCATTGC Db 122 TCGTCCAAAC	Query Match Best Local Similarity Matches 234; Conserv	RESULT 1 US-09-610-185C-3 Sequence 3, Application US/09610 Patent No. 6573432 GENERAL INFORMATION: APPLICANT: Borevitz, Justin APPLICANT: Lamb, Christopher J FITLE OF INVENTION: REGULATION FILE REFERENCE: SALKINS.003C1 CURRENT APPLICATION UNMBER: US/CURRENT APPLICATION UNMBER: US/CURRENT FILING DATE: 2000-07-09 PRIOR APPLICATION NUMBER: US/CURRENT FILING DATE: 2000-06-23 NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows V SEQ ID NO 3 LENGTH: 1033 TYPE: DNA ORGANISM: Arabidopsis thaliana US-09-610-185C-3		34 42.6 5.2 36 42.6 5.2 37 42.6 5.2 38 42.6 5.2 39 42.4 5.1 0 40 41.6 5.0 0 41 41.6 5.0 0 42 41 5.0 0 43 41 5.0 1 5.0 31 44 39.6 4.8 39.6 4.8	9 42.6 9 42.6 10 5.2 10 5.2 10 5.2 10 5.2 10 5.2
TAATCT 332	AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT 318	GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258 	AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA 198 	TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 138 	TCTTCATIGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78	22.5%; Score 186; DB 4; Length 1033; larity 74.5%; Pred. No. 2.8e-39; Conservative 0; Mismatches 80; Indels 0; Gaps 0;	185C OF AN OF (603,)	ALIGNMENTS	5361 3 US-08-973-462-2 Sequence 2, Appli 6152 3 US-08-973-462-1 Sequence 1, Appli 6201 2 US-08-790-912-1 Sequence 1, Appli 15213 4 US-08-961-527-26 Sequence 26, Appl 5889 4 US-09-402-929-3 Sequence 3, Appl 825 4 US-09-402-929-3 Sequence 849, Appl 827 4 US-09-601-198-52 Sequence 52, Appl 19124 2 US-09-601-198-52 Sequence 13, Appl 319608 4 US-09-339-333D-1 Sequence 11, Appli 319608 4 US-09-679-409-1 Sequence 1, Appli 2732 1 US-08-476-000-60 Sequence 60, Appl 2732 1 US-08-472-840-60 Sequence 60, Appl	3 US-08-973-462-3 Sequence 3, 3 US-08-961-083-93 Sequence 93 4 US-09-536-784-93 Sequence 93 3 US-08-961-083-3 Sequence 3, 4 US-09-536-784-3 Sequence 3, 4 US-09-627-122-21 Sequence 21

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RESULT 2
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; TYPE: DNA
; ORGANIEM: Arabidopsis Thaliana
US-09-610-185C-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                           Sequence 1, Application US/08722626B Patent No. 5939601
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                                                                 GENERAL INFORMATION:
APPLICANT: Yang, Yinong
APPLICANT: Klessig, Daniel, F.
APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Borevitz, Justin
APPLICANT: Xia, Xiji
APPLICANT: Xia, Xiji
APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIGMENT
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: SALKINS.003C1
                            CORRESPONDENCE ADDRESS:
                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 21.8%;
Local Similarity 68.0%;
les 251; Conservative
 ADDRESSEE:
STREET: 1
                                                                                                                                                                                                                                                                         442
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3: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
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Pred. No. 8.7e-38;
0; Mismatches 118;
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; LOCATION: 148...981
; OTHER INFORMATION:
US-08-722-626B-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE: FEATURE:
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ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
TELEFAX: 215 563-4044
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NAME: Pat Hagan
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19103-2307
COMPUTER READABLE FORM:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                  534 CAAGT 538
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                                                      TAAGT 388
                                                                                                                             CACTAATCTTCTAAGGAAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATTAACAA 383
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59.2%;
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Pred. No. 8.5e-24;
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US-09-008-979A-2
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                                                                                                                                                                                                                                                                             RESULT 5
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                                                                                                                                                                                             Sequence 2, Application US/09460618
Patent No. 6235482
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.3%;
Best Local Similarity 74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (713) 789-26
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Conner
                                                                     APPLICANT: Conner, Timothy W.

TITLE OF INVENTION: Strawberry Promoters and Genes
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (713) 787-1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77210-4433
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               COUNTRY: USA
ZIP: 77210-4433
                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                   Matches 108;
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                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (713) 789-2679 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     LENGTH: 469
TYPE: DNA
ORGANISM: fragaria x ananassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Kammerer, Patricia A.
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                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:058
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 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 ATAAGCTTCTAGGGAACAGGTAATTA 391
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                            182 GGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTC 241
                                                                                      122 TAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ATAAGCTCTTAGGCAACAGATGGTCA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 GGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 TACTTGCAGGCTTAAACAGATGCAGGAAGAGCTGTAGACTGAGATGGCTGAATTATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 base pairs nucleic acid
                                                                                                                     Conservative
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                                                                                                                                 10.3%;
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                                                                                                                   Score 85.2; DB 4;
Pred. No. 3.4e-13;
0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85.2; DB 3;
Pred. No. 3.4e-13;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MONACO, Daniel A. 480 REGISTRATION NUMBER: 60: REFERENCE/DOCKET NUMBER: 60: TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
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                       268
                                                            531 ACAGAAGAGGACAGGATCATCTATGAAGCACATAAGCGGTTGGGAAATCGTTGGGCA
                                                                                                                                                                                                            414 AAATATGGGCCAAAAAGATGGTCTTTAATTGC---AAAACATTTAAAAGGAAGAATAGGC 470
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o. 6410825
                                                                                           208 GAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA 267
                                                                                                                                                                                                                                                                                                                          28 GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT 87
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EDNESS: single
CTTATTGCTGGTAGACTTCCCGGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACT 327
                                                                                                                                    ÁAGCAGTGTÁGÁGAAAGATGGCATÁÁTCATCTGÁATCCTGAGGTAAAGAAATCTTCCTGG 530
                                                                                                                                                                       AAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGGGACTTT 207
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Hatton, Kimi
Reddy, E. P.
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Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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Pred. No. 2e-12;
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                                                 Matches 160;
                                                             Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 2220 base pair
                                                                                                                                                            FEATURE:
                                                                                                                                                                                            TISSUE TYPE: A IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-JUN-
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PLANT REGULATORY PROTEINS
                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                              NAME/KEY:
LOCATION:
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STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winner, Ellen REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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32 TGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGATAAGT 91
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US-09-402-929-1
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                                                                                                             Query Match
                                                                                                                                                                                                                                            TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Temple
                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TOSCANI, ANTONIO
APPLICANT: HATTON, KIMI
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP:
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                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                           Local
                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A.
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                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 TGAAGAAGGGGCCCTGGACGTCCGCGGAGGACGCCATCCTGGTGGACTACGTGAAGAAGC 458
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                                                                                                                                                                                I: 3602 base pairs
nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philadelphia
: PA
                                                                                         Similarity
GAATTGATAAAGGGTCCTTGGACTAAGGAAGAAGATCAGAGGGTTATTGAATTAGTTCAG
                                   GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SEIDEL, GONDA, LAVORGNA & MONACO, Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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                                                                                         9.4%;
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                                                                                         Score 77.2; DB 4; Pred. No. 8.3e-11;
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                                                                         Mismatches
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                                                                      US-09-402-929-4
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GENERAL INFORMATION:
 Matches
            Query Match
Best Local Similarity
                                                                                                                                                                          TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 6775 base pair
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                      TOPOLOGY: lir
                                                                                                                                                                                                                                                NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                    nucleic acid
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                                                                                                                                       6775 base pairs
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Toscani, Au-
Toscani, Kimi
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Reddy, E.
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 Conservative
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                                                                                      linear
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              9.4%;
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Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                       PCT/US98/06896
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                                                                                                                                                                                                                                                                 30,480
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              Score 77.2; DB 4;
Pred. No. 1e-10;
Mismatches 138;
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                             Length 6775;
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28 GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTTAGGAAAAATGTATTGAT 87

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                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,251
PILING DATE: 23-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO AU96/00383
PILING DATE: 21-JUN-1996
PRIOR APPLICATION DATA;
APPLICATION NUMBER: AU PN6470/95
PILING DATE: 09-NOY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JACOBSEN, JOHN V.
APPLICANT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Boulevard
MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Ory
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN3779/95
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                            TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                       NAME: Winner, Ellen P. REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 5370
CITY: Boulder
                                                                                                                                  LENGTH:
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                                                                                                                                2352 base pairs
                                                                                                                                                                                                      (303)
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  Oryza sativa
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                                                                                    single
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CLESTICALL.

PILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
ATTORNEY KAMMBER: 29,775
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1438
TELEPHONE: (713) 789-2679
TELECHONE: (713) 789-2679
TELECHONE: TELEPHONE: (713) 780-2679
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LOCATION:
US-08-997-251-3
Query Match
Best Local Similarity
Marches 133; Conserve
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                                                                                         TOPOLOGY:
US-09-008-979A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09008979A Patent No. 6080914
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 TGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T: Conner, Timothy W. INVENTION: Strawberr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCCGCTCATTTGCCAGGGCGCACTGATAATGAAATAAAGAATTACTGGAATACT 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Carmen Rodriguez, Paralegal, Arnold, White & Durkee
P.O. Box 4433
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Pred. No. 2.4e-10;
                                  Score 71.4;
Pred. No. 1.
                    Mismatches
                                    .6e-09;
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RESULT 13
US-09-460-618-6
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Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775 REFERENCE/DOCKET NUMBER: MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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340 AAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATT
                                                                              280 AGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTATTGGAACACTAATCTTCTAAGG
                                                                                                                                                         220 GTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGT
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                                                      CGATTGCCAGGAAGAACTGCCAATGATGTGAAGAACTATTGGAATACTTA---TCAAAAGG
                                                                                                                        GTTGATTTGATCAGGCTTCATAAGCTTCTAGGAAACAGGTGGTCTTTAATTGCCGGA
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                                                                                                                                                                                           Score 71.4; DB 3;
Pred. No. 1.6e-09;
0; Mismatches 81;
                                                                                                                                                                                             81;
                                                                                                                                                                                                                            Length 785;
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                                                                                                                                                                                                                                                                                                 Patent No. 5670367
CENERAL INFORMATION:
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CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09310235B Patent No. 6392030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
ZIP: 22313-029
ZIP: 22313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
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TYPE: DNA
ORGANISM: fragaria x ananassa
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OTHER INFORMATION: N = A,
                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                       CITY: Alexandria
                                                                                                                                                                         STREET:
                                                                                                                      COUNTRY:
                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 AAAAAGGATCAAAAGACGGCTTCATACGCAAAGAAACTGAAAGTTAAACCCCGAGAAAAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CGATTGCCAGGAAGAACTGCCAATGATGTGAAGAACTATTGGAATACTTA---TCAAAGG
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                                                                                                                                                                                                                                                                                                                          4, Application US/08232463
5670367
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1800 Diagonal Road,
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Pred. No. 1.6e-09;
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G
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                     Version
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Search completed: January 30, 2004, 08:33:09 Job time : 64 secs
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; CLONE: pTZgpt-F1s
US-08-232-463-14
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.4%; Score 69.6; DB 1; Length 7218;
Best Local Similarity 7.0%; Pred. No. 1e-08;
Matches 30; Conservative 233; Mismatches 167; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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                                                                                                               725 AAAATTGGGG 734
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Database :
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/1/pubpna/US07
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               /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10NEW_PUB.seq:*
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cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Compugen Ltd.
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                                                                                                                                                                                                                                          NEW PUB. seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21090	2010140	,21
179 179 179 170.6 157.4	186 186 186 186 185.4	Score 825 618
21.7 21.7 20.7 19.1	22.5	Query Match 100.0
		Length
112	111 15 11	DB 14
US-09-938-842A-2634 US-09-934-455-437 US-09-878-574-2454 US-09-443-704-5	US-09-734-45-268 US-10-295-403-43 US-10-295-403-43 US-09-934-455-13 US-09-934-455-481 US-09-938-8428-2814	US-10-033-190-1 US-10-033-190-4
Sequence 2634, Ap Sequence 437, App Sequence 2454, Ap Sequence 5, Appli	Sequence 4/9, App Sequence 268, App Sequence 43, Appl Sequence 13, Appl Sequence 481, App Sequence 481, App	Description Sequence 1, Appli Sequence 4, Appli
	21.7 747 12 US-09-938-842A-2634 Sequence 21.7 925 11 US-09-934-455-437 Sequence 20.7 390 10 US-09-878-574-2454 Sequence 19.1 514 9 US-09-443-704-5 Sequence	186 22.5 982 9 US-09-770-445-268 Sequence 2/8, 186 22.5 1016 15 US-10-295-403-43 Sequence 2/8, 186 22.5 1016 15 US-10-295-403-43 Sequence 2/8, 186 22.5 1033 11 US-09-934-455-13 Sequence 43, 185.4 22.5 741 11 US-09-934-455-481 Sequence 481, 185.4 22.5 741 10 US-09-938-842A-2634 Sequence 2/83, 179 21.7 747 10 US-09-938-842A-2634 Sequence 2/83, 179 21.7 747 12 US-09-938-842A-2634 Sequence 2/83, 179 21.7 747 12 US-09-938-842A-2634 Sequence 2/83, 179 21.7 390 10 US-09-878-7574-2454 Sequence 2/45, 157.4 19.1 514 9 US-09-443-704-5 Sequence 5, Ap.

ALIGNMENTS

RESULT 1 US-10-033-190-1

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Sequence 1, Application US/10033190
Publication No. US20020133848A1
GENERAL INFORMATION:
APPLICANT: Exclixis Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARA
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EPO1-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CCURRENT APPLICATION NUMBER: US/0033,190
CCURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION UNMBER: US/0034,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
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; ORGANISM: Lycopersicon esculentum
US-10-033-190-1
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SEQ ID NO 1
LENGTH: 825
                                                                                                                                                                                                                                                                                                             Matches 825; Conservative
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Best Local Similarity
                                            121
181 AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT 240
                                                                                     121 ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA 180
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100.0%; Pred. No. 4e-179;
tive 0; Mismatches 0
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Db 04
                                                                                                                                              APPLICANT: Exelixis Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EP01-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1012
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US-10-033-190-4
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                                                                                                                ; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Lycopersicon
US-10-033-190-4
                                                                     Query Match
Best Local S
Matches 825
                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10033190 Publication No. US20020133848A1 GENERAL INFORMATION:
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                                                                                Similarity
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                         ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGAAGAA
                                               ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
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                                                                   Score 618; DB 14;
Pred. No. 1.2e-131;
0; Mismatches 0;
                                                                                          Length 1012;
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                                                                      187;
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                                             RESULT 3
US-09-934-455-479
Sequence 479, Application US/09934455
Publication No. US20030121070A1
GEMERAL INFORMATION:
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              APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
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                                                                                                                                        ACAAAATGATTTTTTTTTGGAAAATTGACTTATGGAATCTACTTGATTAA 825
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PRIOR APPLICATION NUMBER: 60/27439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID MOS: 516
SOFTWARR: Patentin version 3.1
SEQ ID NO 479
LENGTH: 762
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(630)
OTHER INFORMATION: G2421
US-09-934-455-479
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US-09-770-445-268/c
                                                                                           Sequence 268, Application US/09770445
Patent No. US2002023281A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: An, Yong-Qiang
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Best Local Similarity
                                      APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant
FILE REFERENCE: MSI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGCAGGAAAAGTTGTAGACTAAGATGGTTAAACTATTTGAAGCCAAGTATCAAGAGA
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                                    An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Pilgrim, Marsha
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Jiang, Cai-Zhong
Yu, Yang
Rameaka, Joshua
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US-10-295-403-43
Sequence 43, Application US/10295403
Publication No. US20030101481A1
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Reuber, Lynne Jiang, Cai-Zhong Keddie, James Zhang, James

Pineda, Omaira Broun, Pierre APPLICANT:

Riechmann, Jose Luis Adam, Luc

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NAME/KEY: misc feature
LOCATION: (1)...(982)
OTHER INFORMATION: n = A,T,C or
US-09-770-445-268
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Best Local :
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APPLICANT: Hurban, Patrick
ITILE OF INVENTION: Expressed Sequences of Arabidopsis
ITILE OF INVENTION: Expressed Sequences of Arabidopsis
ITILE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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TGGAACACCCATCT 598
                      TGGAACACTAATCT 332
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                                                                                                                                                                                                CGATGCAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
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                                                                                      AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT 318
                                                                                                                               GGAAGACTTAGCAATGATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAAT
                                                               AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAAATTAC
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Slader, Ted
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Pred. No. 1.2e-32;
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Fromm, Mike

Benito, Maria-Ines

Guo-Liang

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; SEQ ID NO 43
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (96)..(842)
; OTHER INFORMATION: G663
US-10-295-403-43
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FILE REFERENCE: MBI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-12-22
                                                                                                                                                                                                              Sequence 13, Application US/09934455 Publication No. US20030121070A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 234; Conserva
                                                                                  APPLICANT:
APPLICANT:
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APPLICANT:
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SOFTWARE: PatentIn Ver. 2
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  APPLICANT:
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                                                                                Creelman, Robert
Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
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                                          Pilgrim, Marsha
Ratcliffe, Oliver
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Jose Luis
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Pred. No. 1.2e-32;
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TYPE: DNA
COMMANDAM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (113)...(862)
OTHER INFORMATION: G663
US-09-934-455-13
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Adam, Lu
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Best Local Similarity
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PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                  APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
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APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant
FILE REFERENCE: MBI-0025
             APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
                                                                                                         APPLICANT:
CURRENT APPLICATION NUMBER: US/09/934,455
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Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
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                                                                   Riechmann, Jose Luis
Yu, Guo-Liang
                                                                                                       Reuber, Lynne
                                                                                                                        Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
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74.5%;
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Pred. No. 1.2e-32;
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FILING DATE:

2001-08-22

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRA
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, WANG METHODS OF USE
TITLE OF INVENTION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILLING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2634
LENGTH: 747
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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; NAME/KEY: CDS
; LOCATION: (1)..(741)
; OTHER INFORMATION: G2422
US-09-934-455-481
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 481
LENGTH: 741
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Patent No. US20020160378A1
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Best Local Similarity
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PRIOR FILING DATE: 2000-08-22
PRIOR PPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
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                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2634
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2634, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING FILE REFERENCE: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                            Local Similarity
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                          139 AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA 198
130 CGGTGCAGGAAAAGTTGTAGATTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                      233;
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                                                                                    TGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAAC 129
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Pred. No. 4.2e-31;
                                                                                                                                                                                                                                                                          Score 179; DB 12;
Pred. No. 4.2e-31;
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US-09-934-455-437
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SEQ ID NO 437
LENGTH: 925
TYPE: DNA
ORGANISM: Arabidopsis thalian
FEATURE:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
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TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 516
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PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
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                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (59)..(697)
OTHER INFORMATION: G1329
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                                  GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                           AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA 198
                                                                                                                                              TGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAAC
                                                                                                                                                                             TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCCATAAGAGCTGGTCTGAAT 138
                                                                                                                                                                                                                     TCGTCCAAAGGGCTGCGAAAAGGTGCTTGGACTACTGAAGAAGATAGTCTCTTGAGACAG 127
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 GGAAAACTTAGCTCTGATGAAGTCGATCTTCTTCTTCGCCTTCATAGGCTTCTAGGGAAT
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Pilgrim, Marsha
Ratcliffe, Oliver
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Jiang, Cai-Zhong
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Dubell, Arnold
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72.1%;
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Pred. No. 4.6e-31;
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US-09-443-704-5

Sequence 5, Application US/09443704
Patent No. US20020066120A1
GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca APPLICANT: Liu, Zhan-Bin APPLICANT: Odell, Joan

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SEQ ID NO 2454
LENGTH: 390
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Best Local Similarity
Matches 227; Conserv
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Patent No. US2002
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APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(390)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-024-Q1-B1-G6
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                                  340 AAGTTAAATACTACTAAAATTG 361
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                                                                                                                                                          216 GTGGAAATGATAATCAAACTCCATAAATTACTAGGCAACAGATGGTCGTTGATTGCACGA
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                                                                                                                                                                                                                                      156 CTAAGATGGCTGAACTATCTCCGTCCTAACATCAAGAGAGGAAATTTTGCGGAGGAAGAA
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AAACTAAATGTAATAGAAGCTG
                                                                                                      AGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGG
                                                                                                                                                                                               GIGGAICTCATTTIGAGGCTICATAAGCTCTTAGGCAACAGAIGGTCACTTATTGCTGGI 279
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                                                                              AGGCTACCAGGAAGGACTGCCAATGATGTGAAAAACTATTGGAACTGTCATCTGAGCANA
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0020110548A1
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Pred. No. 2.6e-29;
0; Mismatches 95
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (484)
; OTHER INFORMATION: I
US-10-008-118A-5
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US-10-008-118A-5
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LENGTH: 514
TYPE: DNA
CORGANISM: Glycine max
FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: (484)
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10008118A Publication No. US20020187539A1 GENERAL INFORMATION:
                                                                                                                                                  NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.1%;
Best Local Similarity 66.2%;
Matches 227; Conservative
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                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/008,118A CURRENT FILING DATE: 2001-12-05 PRIOR APPLICATION NUMBER: 60/109,294 PRIOR FILING DATE: 1998-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: No. US20020066120Alember 20, 1998 NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Plant MYB-Related Transcription Factors FILE REFERENCE: BB1280 USDIV
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                                                                                                         TYPE: DNA
ORGANISM: Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 CTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 TGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 GCTTACCAAGTATATCCAAGCTCATGGAGAAGGCCAATGGAAAATCACTACCCAAAAAAAGC
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Pred. No. 3.1e-26;
0; Mismatches 116;
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2636
LENGTH: 774
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2636
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
ITTLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2636, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.3
Matches 227; Conservative
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155
                                   152 GTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGGTGACTTTGAAC 211
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                                                                                                                                              35 TGAACAAAGGAGCTTGGACTAAAGAAGAAGATCAGCTTCTTGTTGATTACATCCGTAAAC
                                                                                                                                                                                 32 ТGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGATAAGT
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 GTTGTAGATTGAGATGGATGAATTATCTAAGACCAGATCTCAAAAGAGGCAATTTTACTG
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Pred. No. 1.5e-25;
0; Mismatches 112;
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; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2636
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2636
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Search completed: January 30, 2004, 09:31:32 Job time: 304 secs
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US-09-938-842A-2636
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APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                      332 TTCTAAGGAAGTTAAATACTACTAAAATTGTTCC 365
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                                                                                                       TCAAGAGGAAGCTTCTCAGCCGTGGGATTGATCC
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Post-processing: Minimum Match 0%
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ALIGNMENTS

FEATURES source	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BE462282 LOCUS DEFINITION
Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence. Location/Qualifiers 1. 490	,F., Hansen,T., Craven,M.B., Bowman,C.L., Romning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue, 0-3 mm buds Unpublished Contact: CUGI	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 490) van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang	Lycopersicon esculentum CDNA Cione CTVA12C2, mRNA sequence. BE462282 BE462282.1 GI:9508051 EST. Lycopersicon esculentum (tomato) Lycopersicon esculentum	BE462282 490 bp mRNA linear EST 18-MAY-2001 EST324546 tomato flower buds 0-3 mm, Cornell University

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REFERENCE
AUTHORS
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asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Lycopersicon esculentum cDNA clone
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Email: http://www.genome.
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/dev_stage="0.3mm buds"
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/clone_lbb="tomato flower buds 0-3 mm, Cornell Universit
/note="Vector; pBlueScript SK(-); Site 1: EcoR1; Site 2:
/note="Vector; pBlueScript SK(-); Site 1: EcoR1; Site 2: EcoR1; Site 2:
/note="Vector; pBlueScript SK(-); Site 1: EcoR1; Site 2: EcoR1
organism="Lycopersicon esculentum"
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post-imbibition, Cornell University
clone cLEZ18K18 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE462229 335 bp mRNA linear EST 18-
EST324493 tomato flower buds 0-3 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOA12C3, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
                                                                                                                                                             Clemson University
                                                                                                                                                                                                        Unpublished
Contact: CUGI
                                                                                                                     Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                            100 Jordan Hall, Clemson,
                                                                                                                                                                                     Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (tomato)
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xho1; supplier: Tanks1ey: Tissue supplied
(USDA-ARS, Ithaca, NY 14850)."
79 c 91 g 119 t 1 others
/organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
                                                                            Location/Qualifiers
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/dev_stage="seedlings 5 days post-imbibition"
/clone_lib="comato radicle, 5 d post-imbibiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4081"
/clone="cLEZ18K18"
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/cultivar="TA496"
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Pred. No. 6.5e-39;
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                                                                                                                                                                                                                                                                           1 (bases 1 to 749)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Kozik, A., Michelmore, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ990780
QGF21B10.yg.ab1 QG_EFGHJ
QGF21B10, mRNA sequence.
BQ990780
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] singleton, see http://cgpdb.ucdavis.edu/ for details. Plate: QGF21 row: B column: 10.
                                                                                                                    Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cichorieae; Lactuca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactuca sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ990780.1 GI:22410315
                                                                                                                                                                                                       Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                    http://compgenomics.ucdavis.edu/
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1-(530)-752-9659
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/dev stage="0-3mm buds"
/clone_lib="tomato flower buds 0-3 mm, Cornell University"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

size-separated while remaining frozen."
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/clone="cTOA12C3"
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80.3%;
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Matches 246; Conser
                         TITLE
                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442
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                                                                                                             Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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367 bp mRNA linear EST 19-DEC-2000 NF104H01DT1F1014 Drought Medicago truncatula cDNA clone NF104H01DT 5', mENA sequence.
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Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                               EST
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                                                                                      (bases 1 to 367)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="QG_EFGHJ lettuce serricla"
/note="Vector: pBRCDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_IB=QE_EFGHJ lettuce serricla

TAG_TISSUE=leaves dark grow
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/cultivar="L.serriola"
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Plant Biolo
The Samuel
2510 Sam No
Tel: 580 22
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kin, C., Doyle, M., Brzoska, P., Wongone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: gdmay@noble.org
Insert Length: 367 Std Error: 0.0
Plate: 104 row: H column: 01
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                           AI995124 486 bp mRNA
701502113 A. thaliana, Ohio State clone
CDNA clone 701502113, mRNA sequence.
                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; euroside II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 486)
                                                                                                                                     Arabidopsis thaliana (thale cress)
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It Biology Division

Samuel Roberts Noble Foundation

Samuel Roberts Noble Foundation

Sam Noble Parkway, Ardmore, OK 73402,

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580 221 7380
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1. .367
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/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/clone_lib="Drought"
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/mol_type="mRNA"
/db_xref="taxon:3880"
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Rosa hybrid cultivar
Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside;
; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turner, C., Krikorian, S., Elder, L. and Hanson, D. Arabidopsis thaliana Gene Expression MicroArray Unpublished
Rose Scent: Genomics Approach to Discovering Fragrance-Related Genes Plant Cell 14 (10), 2325-2338 (2002) Contact: Naama Menda
                                                                                                                          i (bases 1 to 427)
Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M., Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J., Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and W.
                                                                                                                                                                                                                                                                                                                                                        BQ105368
BQ105368.1 GI:20155030
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ105368 427 bp mRNA linear EST : fc0707.e Rose Petals (Fragrant Cloud) Lambda Zap Express Rosa hybrid cultivar cDNA clone fc0707.e 5', mRNA sequence
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4633 World Parkway Circle, St.
Tel: 877-577-2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Systems, Inc., a wholly owned subsidiary of Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: service@genomesystems.com
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/note="CDNA library was made from selected clones
Arabidopsis thaliana Ohio State clone set."
a 83 c 111 g 144 t
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/db_xref="taxon:3702"
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74.2%;
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No. 9e-26;
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KEYWORDS
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Best Local Similarity
Matches 243; Conserv
                                             AUTHORS
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                                                   Rosa hybrid cultivar

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core et
; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

1 (bases 1 to 488)

1 (bases 1 to 488)
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  Guterman,I., Shalit,M., Menda,N.,
Shalev,G., Bar,E., Davydov,O., Ova
,Z., Pichersky,E., Lewinsohn,E., Z
                                                                                                                                                                                                  gg1664.e Rose Petals (Gr
hybrid cultivar cDNA cla
BQ105048.
BQ105048.1 GI:20154710
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Seq primer: T3 forward.
                                                                                                                                                               Rosa hybrid cultivar
                                                                                                                                                                                                                                                                                                                                                                                   ⊢]
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/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"
82 c 111 g 92 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Fragrant Cloud"
/db_xref="taxon:128735"
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Pred. No. 2.1e-23;
"' smatches 118;
                                                                                                                                                                                                                                                            488 bp
(Golden Gate)
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N., Piestun,D., Dafny-Yelin,M.,
Ovadis,M., Emanuel,M., Wang,J.
., Zamir,D., Vainstein,A. and W
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Lambda Zap Express Library Rosa
s 5', mRNA sequence.
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    Wang,J., Adam
A. and Weiss
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Rosa hybrid cultivar
Rosa hybrid cultivar
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosid
                                                            BQ104423 508 bp
gg0628 e Rose Petals (Golden Gate)
hybrid cultivar cDNA clone gg0628.e
BQ104423
BQ104423.1 GI:20154085
EST.
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Fax: 972 8 9468 263
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Plant Cell 14 (10), 232
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Rose Scent:
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Seq primer: T3 forward.
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/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Golden Gate) Lambda
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/strain="Golden Gate"
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/clone="gg1664.e"
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Pred. No. 2.1e-23;
0; Mismatches 118
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1 (bases 1 to 508)
Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M., Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J., Adv, R., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weiss
                                 BM092559 551 bp mRNA linear EST 29-NOV-2 sah15d11.y3 Gm-c1086 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1086-1342 5' similar to TR:023891 023891 OSMYB3. ;, mRNA
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. Box 12, Rehovot, 76100, Israel
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/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Golden Gate) Lambda Zap Express
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further is call: (800)-533-4363 or contact via email: ccu@resgen.com
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Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; rosids
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GCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCA
                                                                                                                    AAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAG
                                                                                                                                                                           GAGAAGCCCTTGTTGTTCAAAGGAGGGTTTGAATAGAGGTGCTTGGACAGCTCATGAAGA
                                                                                                                                                                                                                                                                                                                                                    GAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGA
                                                          AAGAGCAGGTTTGAAAAAGATGTGGAAAAAGTTGCAGACTTAGATGGTTGAATTATCTCAG
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/CIONE LIDE GIM-CLOOD
/CIONE LIDE GIM-CLOOD
/CIONE LIDE GIM-CLOOD
XhoI; The cDNA library was constructed from mRNA isolated
from very young seeds (less than 20mgs). The library was
prepared using the Stratagene pBluescript II SK (+)
library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an Xho I restriction site. Eco RI
adaptors were ligated to the blunt-ended cDNA fragments
followed by Xho I digestion. The cDNA insert is protected
from Xho I digestion via methylation during first strand
cDNA sythesis. The cDNA fragments were directionally
cloned into the Eco RI-Xho Irestriction site of the
pBluescript vector. The ligated cDNA fragments were
pBluescript vector. The ligated cDNA fragments were
library was constructed by Anu Khanna (Lila Vodkin lab,
University of Illinois)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="young seeds
/lab_host="DH10B"
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'tissue_type="young seeds (Williams 82)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Glycine max"
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                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 165.8; DB:
Pred. No. 3.6e-22
0; Mismatches 11;
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ORGANISM
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CA410578
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                              249;
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843_F -P proteoid r
5', mRNA sequence.
CA410578
19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: AATTAACCCTCACTAAAGGG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 612 624 6765
Fax: 612 625 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Uhde-Stone, Claudia
Department of Agronomy and Plant Genetics
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roots of white lupin in response to P deficiency Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allan, D.L.

Nylon filter arrays reveal differential gene expression in proteoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lupinus albus (white lupine)
Lupinus albus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cuhde@soils.umn.edu
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAATAAAGAATTATTGGAACACCAATTTAGGAAAAAAGGTGAA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 494)
                                                                                                                                                //dev stage="12 and 14 DAE"
//dev stage="12 and 14 DAE"
//clone lib="-p proteoid root (cluster root); Vector:
//note="Organ: -P proteoid root (cluster root); Vector:
//note="Organ: -P proteoid root (cluster root); Vector:
pBLUESCRIPT SK(+/-); Site 1: EcoRI; Site 2: XhoI; Proteoid
roots of white lupin grown under P deficient conditions
were harvested 12 and 14 DAE (days after emergence), and
poly(A)+ RNA was isolated. The poly(A)+ RNA obtained from
plants 12 and 14 DAE was combined in a 1:1 ratio and 7 ug
total RNA was used for reconstruction of a proteoid root
cDNA library in the phage ZAPII vector according to the
manufacturer's instructions (Stratagene, La Jolla, CA, USA
). For conversion of the phage library into the plasmid
form, mass excision was performed according to the
procedure described by Stratagene."
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                                                                                                                                                            197
                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:3870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="ultra"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Lupinus albus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="843"
                                                                              20.1%;
                                                                              Score 165.6; DB 14; Pred. No. 3.9e-22;
                                                              Mismatches
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                                                                                                  494;
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                                                                                                                                                                                                                                                                                      Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman, T., deBruijn, F.J.,
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                                                                                                                                                                                                                                                                                                                                Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                Lansing, Mi
Tel: 517-353-0854
                                                                                                                                                                                                                                                                                                                                                                                    MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                          Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7846151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Reegstra, Kende, H., L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., E. and Somerville, C.
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                                                                                                                                    /clone_lib="Lambda-PRL2"
                                                                                                                                                                                                                /organism="Arabidopsis
/mol_type="mRNA"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                          db_xref="taxon:3702"
                                                                                                                                                                                            strain="var columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:1053271
                                                                                                                                                                                                                                                      .587
                                                                                                                                                                                                            type="mRNA"
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104 TATATTCAAGCTCATGGAGAAGGCCAATGGAAATCACTACCAAAAAAGGCTGGGCTTCTT 163
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                                                                                                                                                                                                                                                                                                         GGTAACATAACTCCAGAAGAAGATGATCTCATCATCAGAATGCATTCTCTTCTTGGAAAT
                                                                                                                                                                                                                                                                                                                                                         GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTTGAGGCTTCATAAGCTCTTAGGCAAC
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TGGAACACCCATTTATACAAAAAGATGAGAAATCAAGGAACAGATCTAGAAGAAGAATCT
                                                                       TGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATT 378
                                                                                                                                                      AGGTGGTCCCTTATAGCCGGAAGAATACCCCGGACGAACAGATAATGAAATAAAGAACTAT
                                                                                                                                                                                                                              AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
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403
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587 bp mRNA linear EST 30-DEC-1997
psis thaliana cDNA clone 193M15T7, mRNA

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 587) McIntosh

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)

/note-Tvector: lambda Zip-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and 7

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RESULT 13
BG881996
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                                                                                                                         Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1212 Std Error: 0.00
High quality sequence stop: 373.
                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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sae92f10.y1 Gm-c1065 Glycine max CDNA Clone GENOME SYSTEMS
ID: Gm-c1065-3356 5' similar to TR:Q40920 Q40920 MYB-LIKE
TRANSCRIPTIONAL FACTOR MBF1. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max
                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway,
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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a 106 c 135 g 167 t 14 others
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID:
                                                                                                           Location/Qualifiers
                                                                  organism="Glycine max"
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                781 bp mRNA linear EST 15
T008E08 Populus apical shoot cDNA library Populus tremula
tremuloides cDNA 5 prime, mRNA sequence.
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Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
Tel: +46 90 786 5279
Fax: +46 90 786 6676
                                                                                                                                                                              Unpublished
Contact: BHALERAO RUPALI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU830456.1
EST.
                                                                                                                                                                                                                                                     from multiple libraries
                                                                                                                                                                                                                                                                                       The poplar tree transcriptome:
                                                                                                                                                                                                                                                                                                                            Unneberg, P.,
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neberg, P., Bhalerao, R.R.,
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//clone lib="Gm-cl065"

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BU827658
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Department of Plant Physiology
University of Umea, 901 87 Umea,
                                                                                                                                                                                                                                                                                                                                                        Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids I; Malpighiales; Salicaceae; Populus.
1 (Dases 1 to 636)
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Fax: +46 90 786 6676
Email: rupali.bhalerac@plantphys.umu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    Unpublished
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/db xref="taxon:47664"
/tissue_type="apical shoot"
/clone_lib="Populus apical shoot cDNA library"
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                                                      /organism="Populus tremula
/mol_type="mRNA"
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                                                                            ORGANISM
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 JOURNAL
                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                        CDS
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                                                                                                      AF146704.1
                                                                                                                       complete cds.
                                                                                                                                       AF146704
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Petunia integrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 865)

Quattrocchio,F., Wing,J., van der Woude,K., Souer,E., de Vetten,N.,
Mol,J. and Koes,R.
Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
                                                                              Petunia integrifolia
Petunia integrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-APR-1999)
1087, Amsterdam 1081HV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quattrocchio, F., W
Mol, J. and Koes, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular analysis of the anthocyanin2 in the evolution of flower color
                                                                                                                                                                                                                                                                                                                Petunia integrifolia An2
                                                                 Mol, J. and Koes, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCTCATTTTGAGGCTTCATAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSTSNASTSGVRKGAWTEEEDLLLRECIEKYGEGKWHLVPVRAG
LNRCKKSCRLRWLNYLRPHIKGGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGGTAND
VKNYWNTHLRKKLIAPHDQKQESKNKAMKITENSIIKPRPRTFSRPAMNHVSCWNGKS
CNKNYTIDKNEGDTEIIKFGDEKQKPEESIUDGLQWWAANLLAANNIEIEELVSYNSPTLL
HEETAPSVNAESSLTQEGGGGLSDFSVDIDDIWDLLS"
133 c 193 g 229 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="An2 protein"
/protein_id="AAF66728.1"
/db_xref="GI:7673086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="an2"
/allele="an2-S9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="petal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4103"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mol_type="mRNA"
cultivar="S9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26;
Pred. No.
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Netherlands
                                                                                                                                                                                                                                                                                                              866 bp mRNA linear PLN 01-MAY-2000 protein (an2) mRNA, an2-S6 allele,
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edons; core e
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                                              of petunia and its role
                                                                                       Souer, E.,
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                                                                                                                                                a; Tracheophyta;
eudicots;
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                                                                                       de Vetten, N.,
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MEDLINE
PUBMED
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ORGANISM
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VERSION
KEYWORDS
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AF146706
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                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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JOURNAL
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MEDLINE
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                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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10449578
                                                                                                                                                                                                 Petunia x hybrida
Petunia x hybrida
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 868)
1 (bases 1 to 868)
1 (pattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.,
Colatrocchio, F., Wing, J., van der Woude, K.,
                                                                                                                                                                                                                                                                                                                                                                           AF146706 868 bp
Petunia x hybrida An2 truncated
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Submitted (29-APR-1999) Genetics, Vrije Universiteit, 1087, Amsterdam 1081HV, Netherlands Location/Qualifiers
                                                            Quattrocchio, F., W. Mol, J. and Koes, R.
                                                                                                                                        Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-APR-1999)
                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                 AF146706.1 GI:7673091
                                                                                                                                                                                                                                                                                                                                                              complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                 AF146706
                                                                                                            0449578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCTCATTTTGAGGCTTCATAAGCT 259
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                                                                                          (bases 1 to 868)
                                                                                                                                                                                     J. and Koes,R.
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134 c 195 g 227 t
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/db_xref="GI:7673088"
/db_xref="GI:7673088"
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LNRCRKSCRLRWLNYLRPHIKRGDFSUKKAKAKITENNIIKPRQTFSRPAMMHVSCWNGKS
VKNYWNTHLRKKLIAPHDQKQESKNKAKAKITENNIIKPRQTFSRPAMMHVSCWNGTLL
CKNTIDKNEGDTEIIKFSDEKQKPEESIDDGLQWWANLLANNIEIEELVSCNSPTLL
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'chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
cultivar="S6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allele="an2-S6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Petunia integrifolia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="petal limb"
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100.0%;
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                                                                             Wing, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26;
Pred. No.
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                                                                             der Woude, K.,
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protein
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                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                           linear (an2) mRNA,
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                                                                                                                                                                        of.
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                                                                             Souer, E.,
                                                                                                                                                                       petunia
                                                                                                                                                                                                                                                                                                                                                                             PLN 01-MAY-2000 an2-W22 allele,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                             Vetten, N
                                                                                                                                                                          its role
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                                                                                                                                                                                                                    PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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KEYWORDS
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AF146702
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ORIGIN
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Best Local
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                                                                                                                                                                                                      AUTHORS
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234 GATCTCATTTTGAGGCTTCATAAGCT
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Petunia x
                                                                                                                                                                  2 (bases 1 to 1034)
Quattrocchio, F., Wing, J.,
Mol, J. and Koes, R.
Direct Submission
                                                                                                                                                                                                                                                                                                         Submitted (29-APR-1999) Genetics,
                                                                                                                                                                                                                                                    Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
                                                                                                                                                                                                                                                                                                                                                                                 Petunia x hybrida
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AF146702.1
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                                                                                                                                          Amsterdam 1081HV,
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LNRCRKSCRLRWLNYLRPHIKRGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTAND
VKYVWNTHLRKKLIAPHDQKQESKS"
                                                                  /organism="Petunia x hybrida"
/mol_type="mRNA"
/cultivar="V26"
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/product="An2 truncated |
/protein_id="AAP66731.1"
/protein_id="GI:7673092"
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/gene="an2"
             tissue_type="petal limb"
                                         /db_xref="taxon:4102"
/chromosome="6"
                                                                                                                          location/Qualifiers
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/cultivar="W22"
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'chromosome="6"
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AF371977
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AF371977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1339)
Stracke, R., Werber, M. and Weisshaar, B.
The R2R3-WYB gene family in Arabidopsis thaliana
Curr, Opin. Plant Biol. 4 (5), 447-456 (2001)
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                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-APR-2001) Dept. Plant Breeding and Yield Physiology
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Location/Qualifiers
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nilarity 100.0%;
Conservative 0
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VKNYMNTHLRKKLIAPHDOKOESKOKPEESIDDGLGWWANILANNIEIEELVSCNSFTLL
HEETARSVNAESSLTGGGGSGLSDFSUDIDDIWDLVS"
/translation="mgrapccekiglkrgrwTaeeDeilTkyIqtngegswrslpkka
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                                            /product="putative transcription factor"
/protein_id="AAK97396.1"
/db_xref="GI:15420626"
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                                                                                                                  /gene="At5g49330"
/note="ATMYB111; R2R3-MYB family member"
                                                                                                                                                                      gene="At5g49330"
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                                                                                                                                                                                                        'gene="At5g49330"
                                                                                                                                                                                                                                                                                         organism="Arabidopsis
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                                                                                                                                                                                                                                       note="ecotype: Columbia"
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                                                                                                                                                                                          . 85
                                                                                                                                                                                                                                                         _type="mRNA"
_xref="taxon:3702"
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Query Match
Best Local
                                                                                                         source
                                                                                                                                                                                                                                                                                                            Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MIF21
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail.1.3)),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
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AB023039 BA000015
AB023039.1 GI:4220638
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryophyta; Tracheophyta;
Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute, Department of Plant Gene Research; 1532-3, Y Kisarazu, Chiba 292-0612, Japan (E-mail:ynakamu@kazusa. Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P1 and TAC clones
DNA Res. 7 (1), 31-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural analysis of Arabidopsis thaliana chromosome 5. Sequence features of the regions of 3,076,755 bp covered
                                                                                                                                                         shorter because we remove overlaps between neighboring The 5' clone is MDN11 and the 3' clone is K23F3.
                                                                                                                                                                                       This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
                                                                                                                                                                                                                                    Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-FEB-1999) Yasukazu Nakamura, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H.
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/gene="At5g49330"
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                         /mol_type="genomic DNA"
/strain="Columbia"
                                                                           organism="Arabidopsis"
                                                                                                                             ocation/Qualifiers
db_xref="taxon:3702"
                                                                                                            . .59372
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/number=7 /evidence=not_experimental complement(54445503)	unknown protein" /number=8 /number=8 /evidence=not_experimental complement(50625250) /note="CDS is reported in Acc# AB017064 gene_id:MNN11.21 unknown protein"	unknown protein" /number=9 /evidence=not_experimental complement(49104963) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21	complement (43674453) /note="CDS is reported in Acc# AB017064 gene id:MDN11.21	/number=11 /number=11 /evidence=not_experimental complement(35614266) /note="CDS is reported in Acc# AB017064 gene_id:MNN11.21 unknown protein" /number=10 /evidence=not_experimental	/number=12 /number=12 /evidence=not_experimental /evidence=not_experimental complement(30333412) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.1	/number=13 /evidence=not_experimental complement(28312952) /note="CDS is reported in Acc# AB017064 gene_id:MDNI1.21 unknown_rotein"	unknown protein" /number=14 /evidence=not experimental complement(21612266) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"	/number=15 /number=16 /number=16 /evidence=not experimental /evidence=not experimental complement(1273, 2061) /note="CDS is reported in Acc# AB017064 gene_id:WDN11.21	/number=16 /number=16 /evidence=not experimental /evidence=not experimental complement(770845) /note="CDS is reported in Acc# AB017064 gene_id: MDN11.21 unbody reported."	/number=17 /number=17 /number=17 /evidence=not_experimental complement(587698) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 introvar protein"	/number=18 /number=18 /number=18 /evidence=not experimental complement(109263) /note="CDS is reported in Acc# AB017064 gene id:MDN11.21	complement(130) /note="CDS is reported in Acc# AB017064 gene id:MINI1.21
CDS			CDS			CDS	exon	exon	exon	exon	exon	· .
S complement (join(14112. 14562,1464715668)) /note="gene_id:MIF21.4"		/codon_start=1 /evidence=not_experimental /product="polygalacturonase" /protein_id="BAA9694.1" /db_xref="01:8777404" /translation="MGRVHFGVSAFFVFCLLGLSANAKIFNINSPPGSDITNALLKAF	\ L 0 5	MIKOLITOLPRE FEKXI IGSLARQENKERYVSPLVALYASKSVI PEGGOTNOLI ARGULA VORCI ESTANDI INCLINGOLI MIKOLITOLPRE FEKXI IGSLARQGINKERYVSPLVALYASKSVI PEGGOTNOLI ARALD LLLTROKAYREVPVGFYFACLAHNIKHDTVLKLQDQI VSLLHTAQPENF I YPKAGNRQ VAFSQELLTWESLFSVYVSTESERHLTSSSSINVRVGKLMDI FILSRLEYDQENKTTRF I ELI ETVPMSFRESHDQLYLAVNAFIQVHTNI SQEEKGS I CSYLNCQKLSQEASLELVK NEKWPLRILVYQALFIQQLNTHQAFKDCSDSFRFTNSADFSGSVVPSSRPLTSQQSPCT DDETGPRNR PLCFLMQKDATLDEFESTSFR I HNLEEQLVSLKKSLHSHDNLKKPNCLG KRSASRNKNTFGQVTTACI GSVSFTSQRKYANRLLQI LRRVNLFGSRKTNR SKAGESE B"	/protein id="BAA9693.1" /protein id="BAA9693.1" /db_xref="dI:8777403" /translation="METFSLKDCSSVASSPISSPNISTLLKIKVLSWSKETGLPASVH /translation="METFSLKDCSSVASSPISSPNISTLKIKVLSWSKETGLPASVH VRVCNKSFNLHKSLLCAKSGYFKEREDQLSEIEIPOEFPGGAETFEKIMLFIYGCPTL VHPNNIAGLRCAAQFLEMTEQHTSNLCEREDLYLNQVVLQNWDDTLVVLKKCQDLVP	/evidence=not join(790680 join(790680 /note="contail gene_id:MIF21. /codon_start=1 /evidence=not	/number=2 /evidence=not_experimental /evidence=not_experimental complement (63156389) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein" /number=1	- T ID > O > >	~ E W ~ O ~ ^	~ E 10 ~ 0 ~ ^	- C (0 > 0 >)	/note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"

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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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norvegicus clone CH230-15207, WORKING DRAFT SEQUENCE,
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On Sep 19, 2002 this sequence version replaced gi:21745861.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved
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Center clone name: CH230-15207
Center clone name: CH230-15207
Center clone name: CH230-15207
Assembly program: Phrap; version 0.990329
Consensus quality: 223122 bases at least Q30
Consensus quality: 224872 bases at least Q30
Consensus quality: 224872 bases at least Q30
Consensus quality: 225979 bases at least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                      /note="clone_boundary
clone_end:Sp6
site:EcoRI
                          end_sequence:BH336082"
30867. .33254
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/note="clone_boundary
clone_end:T7
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     /note="wgs_end_extension
                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                             'clone="CH230-15207"
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                                                                                                                                                                              sequence:BH336083"
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                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-APR-1999) Genetics, V. 1087, Amsterdam 1081HV, Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                     Mol, J. and Koes, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 865)

1 (bases 1 to 865)

1 (bases 1 to 865)
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Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 11 (8), 1433-1444 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_end_extension
clone_end:T7"
38121: .39480
/note="wgs_end_extension
clone_end:T7"
a 42956 c 44454 g 70267
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34423. .38020
 /note="nonsense mutation"
/replace="c"
136 c 195 g 229
                                                                    /trānslation="mstsnastsgvrkgawteeedlllreciekygegkwhlvpvrag
LNRCRKSCRLRRLNYLRPHIKRGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTDLRKKLIAPHD"
                                                                                                           /codon_start=1
/product="An2 truncated protein"
/protein_id="AAF66734.1"
/db_xref="GI:7673098"
                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                      'gene="an2"
                                                                                                                                                                                                                                               'gene="an2"
                                           gene="an2"
                                                                                                                                                                                      note="anthocyanin regulator; myb-related transcription
                                                                                                                                                                                                                              allele="an2-S7"
                                                                                                                                                                                                                                                              tissue_type="petal limb"
. .865
                                                                                                                                                                                                                                                                                       db_xref="taxon:33119"
chromosome="6"
                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
cultivar="S7"
                                                                                                                                                                                                                                                                                                                                               organism="Petunia axillaris"
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An2 truncated
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               170
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1 (bases 1 to 868)

Ouattrocchio, F., Wing, J., van der Woude, K. Somer F. A. Viriania.
                                          . Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-APR-1999) Genetics, V: 1087, Amsterdam 1081HV, Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol, J. and Koes, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 868)
Quattrocchio, F., Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular analysis of the anthocyanin2 gene in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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TGAATTATCTAAGGCCACATAT 191
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LNRCRKSCRLRWLNYLRPHIKRGDFSLDEVELILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTHLRKKLIAPHDQKQESKS"
                                                                                                           /replace="nnnn"
137 c 195
                                                                                                                                                 gene="an2"
                                                                                                                                                                                                                   /protein_id="AAF66732.1"
/db_xref="GI:7673094"
                                                                                                                                                                                                                                           codon_start=1/product="An2 truncated protein"
                                                                                                                                                                                                                                                                                                                                         gene="an2"
                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:4102"
chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                             cultivar="W44"
                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Petunia x hybrida"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                            allele="an2-W44"
                                                                                                                                     note="causes frameshift leading
                                                                                                                                                                                                                                                                                    note="anthocyanin regulator; myb-related
                                                                                                                                                                                                                                                                                                                                                                tissue_type="petal limb"
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                                                     2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                         type="mRNA"
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Pred. No. 4.6;
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Pred. No.
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protein
                                                     DB
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                                          0,
                                                                  Length 868;
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(an2) mRNA,
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                                                                                                                                     to truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of petunia and its role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Souer, E.,
                                                                                                                                                                                                                                                                                      transcription
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                                          0;
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AUTHORS
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                                                                                                                           170
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 909)
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AC097536 Homo sapiens BAC clone AC097536 AC032034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol, J. and Koes, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular analysis of the anthocyanin2 gene of petunia and its role in the evolution of flower.color Plant Cell 11 (8), 1433-1444 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol,J. and Koes,R.
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                                                                                                                                                                   Similarity
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                                                                                                                         TGAATTATCTAAGGCCACATAT 191
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                                                                                                                                                     2.7%; So larity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amsterdam 1081HV, Nethe 
Location/Qualifiers
                                                                                                                                                                                                                            /replace=""
137 c
                                                                                                                                                                                                                                                                                                  VKNYWNTHLRKKLIVPHDQKQESKTKP"
                                                                                                                                                                                                                                                                                                                                    /product="An2 truncated protein"
/protein_id="AAF66730.1"
/db_xref="GI:7673090"
                                                                                                                                                                                                                                                                                                            /trānblation="mstsnastsgvrkgawteeedlillreciekygegkwhlvpvrag
lnrcrkscrlrwlnylrphikrgdfsldevelilrlhkllgnrwsliagrlpgrtand
                                                                                                                                                                                                                                                   /gene="an2"
/note="causes frameshift leading
                                                                                                                                                                                                                                                                                                                                                                                                                      gene="an2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="an2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="petal limb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:4102"
chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Petunia x hybrida"
                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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Submitted (18-OCT-2001) Genome Sequencing Center, Washington
Submitted (18-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Cedroni,M., Haglund,K. and Creason,K.
The sequence of Homo sapiens BAC clone Unpublished (2001)
                                                                                                                                                        Submitted (12-JUN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Feb 9, 2002 this sequence version replaced gi:16902008.
                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                               Submitted (09-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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Waterston, R.H.
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Sulston, J.E. and Waterston, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG.
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                                                                                                                                                                                                                                                          (bases 1 to 194553)
          Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------- Summary Statistics
Center project name: H_NH0803N05
Drafting Center: WIBR
                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
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Missouri 63108,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >> 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

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Location/Qualifiers
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            rpt_family="MaLR" 2241. .22262
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0860. .10912
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db_xref="taxon:9606"
chromosome="2"
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                        ACL30926 219481 bp DNA linear
Rattus norvegicus clone CH230-39011, WORKING DRAFT
ACL330926
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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39462. .39722
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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garra, M., Guerra, W., Guerra, W., Gabisi, A., Ganta, R., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Holling, S., Hullyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Liu, J., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheihwari, M., Mahindartne, M., Mahrud, M., Malty, K., Mangum, B., Mapua, P., Martin, R., Martin, R., Martinez, E., Mangum, B., McLeod, M. P., McNeill, T. Z., Meenen, E., Mangum, B., McLeod, M. P., McNeill, T. Z., Meenen, E., Mangum, A., Mangum, S., McLeod, M. P., McNeill, T. Z., Menen, E., Murphy, M., Nair, L., Morris, S., McLeod, M. P., Mertin, R., Martin, R., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, K., Pannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, K., Regier, M. A., Shert, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Sohaerer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shen, H., Steinle, R., Sosa, J., Sutton, A., Sutton, A., Svatek, S., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trabor, P., Taylor, C., Taylor, C., Wallson, R., Willson, R., Willson, R., Willson, R., Willson, R., Willson, R., Wallson, R., Wallson, R., Wallson, R., Saith, D., R., Holt, R., Woon, L., Woon, L., Woon, L., Woon, L., Won, L., Woon, 
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23264859.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-AUG-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA bases 1 to 219481)
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                                           AC103077.5 GI:25188654
HTG; HTGS_PHASE1; HTGS_DRAFT;
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                           AC103077 220494 bp DNA linear HTG 23-N
Rattus norvegicus clone CH230-224J5, WORKING DRAFT SEQUENCE,
Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                  AGAAGATGAAGAGGTTGTAATT 126595
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1 219481: contig of 219481 bp
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                                                                                                                                                                                                                                                                                                                                                                                                AGAAGATGAAGAGGTTGTAATT 624
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Assembly program: Phrap; version 0.990329
Consensus quality: 213455 bases at least Q40
Consensus quality: 213451 bases at least Q30
Consensus quality: 215564 bases at least Q20
Estimated insert size: 234277; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig describ in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separal by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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The sequence
                                                                                                                                                                                                                                                                                                                                              of Molecular and Human Genetics, Baylor Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-NOV-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine,
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RESULT 14
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Haemophilus influenzae Rd
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U32791.
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                                                                                                      genome
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                               AGAAGATGAAGAGGTTGTAATT 624
                                                                                                                                                                                                                                                                                                                                                                                         74689
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                     L42023
                                                                                                                                                                                                                                                                                                                                                                                     /note="wgs_contig"
a 43966 c 42534 g 58135 t
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_contig"
6265. .8020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                     GI:1574662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="CH230-224J5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6164: contig of 6164 bp in length
6264: gap of unknown length
216851: contig of 210587 bp in length
216951: gap of unknown length
218096: contig of 1145 bp in length
218196: gap of unknown length
218196: gap of unknown length
219324: contig of 1028 bp in length
219324: gap of unknown length
219324: gap of unknown length
220494: contig of 1170 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .220494
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _type="genomic DNA"
_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                Score 22;
Pred. No.
                                                                                                                      Rd section
                                                                                                                                        10913 bp
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Pasteurellaceae; Haemophilus.

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REFERENCE
AUTHORS
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AUTHORS
TITLE
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. gratefully acknowledge the work of Tatusov et al. We have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae deduced from whole-genome comparison with Escherichia coli Curr. Biol. 6 (3), 279-291 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (bases 1 to 10913) White,O., Clayton,R.A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-JUL-1995) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-MAY-1998) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponding H. influenzae genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medical Center Dr, Rockville,
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te,O., Clayton,R.A.,
erson,J., Hickey,E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ical Center Dr, Rockville, MD 20850, USA whole genome was shifted by 588 nucleotides for a new start ct 1, 1996 this sequence version replaced gi:1221866.

Location/Qualifiers
                                                                            /translation="MFKLKSVNLQVYIMLIAIAVIMAFFSVATDGAYLSARNISNLLR
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DIAGVILGGIAVIGFVLWGNYQRRSRQQLQLEVSALSKDFTKYALFAVIVLGAIYLLN
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                            MNGVLVAIAGLILSARLGAGSPSAGQNAELDAIAACVIGGASLAGGVGSVFGVVIGAL
IIASLDNGMSMLDVPTFWQYIVKGGILLLAVWIDTSNKKKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (168. .1295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (168. .1295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HI1109"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="HI1109"
                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .10913
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Dodson, R. and Gwinn, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kerlavage, A.R. and Fleischmann, R.D.
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     .2810)
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GFNFDAKIRRQSIDFYDLFYAHIGAIDVLALSLKRAAKMLQEETLQKIVNERYAGWNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKLFRKGQMKVLDPLIASGKIKVVGDQWVDSWLAEKALQIMENALTANKUNVDAVVAS
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/protein (xylf)"
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/db_xref="GI:1574665"
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DINVSFSLHEGEILGVAGLVGSGRTDMVQCLRGSYEGKREGNIEINQKQVNIKACAQAI
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VKTFSPDLPIGRLSGGNQQKAILAKCLSLNPKILILDEPTRGIDVGAKYEIYLLINQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (1299. .2810)
/gene="HI1110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence similarity; putative"
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LGNEITHKGLTADNEMYLRCKNLLQQVQLDADPNTRVGELGLGQQQLVEIAKALNKQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:148279 percent
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/transl_table=11
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PID:1789990 percent identity: 75.99; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HI1111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HI1111"
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/transl_table=11
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                                                                                                                                                              codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                               'gene="HI1113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to GB:X04691 SP:P00944 GB:K01996 GB:S68257 D1111148279 percent identity: 71.30; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="HI1112"
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                                                                                                                                                                                                                               dentified by sequence
                                                                                                                                                                                                                                                                  note="similar to
                                                                                                                                                                                                                               PID:2293419 percent identity: 52.56; sence similarity; putative"
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REFERENCE
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                                   Utterback, T., McDo
Venter, J.C. et al
Complete genome so
                                                                                                                       Treponema pallidum

Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

1 (bases 1 to 26849)

1 (bases, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton, G.G., Dodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J., Khalak, H., Richardson, D., Howell, J. K., Chidambaram, M., Khalak, H., Richardson, D., Howell, J. K., Chidambaram, M., Chitaman, M., Chidambaram, M., Chidambaram
                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum section AE001227 AE000520 AE001227.1 GI:3322797
                                                                                                                                                                                                                                                                                                                                                                        Treponema pallidum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HI1116"
8594. .9265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HI1114" complement (7001. .7927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWFRQNYPDKFANIRKIMLPHDYLNYWLTGKFCTEFGDASGSGYFDVVKREWKREVFK
YLAPELNMDEVLPKLLSAEQKIGVIKPEIATLFGFNENVIVSTGGGDNMMGAIGTGNI
REGIATMSLGTSGTLVAYTQKPLLNLPPMIANFCSSNNGWLPLVCVMNITSSNKQLMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFAEFFG"
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QGNTFSLESLDQNKPTLLYFWGTWCGYCRYTSPAINSLAKEGYQVVSVALRSGNEADV
NDYLSKNDYHFTTVNDPKGEFAERWQINVTPTIVLLSKGKWDLVTTGLTSYWGLKVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to PID:1213065 SP:P52229 percent identity:
36.36; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNIWCWQNGISGIYNLGTGNAESFRAVADAVVKFHGKGEIETIPFPEHLKSRYQEYTQ
ADLTKLRSTGYDKPFKTVAEGVTEYMAWLNRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIIVTGGAGFIGSNIVKALNDLGRKDILVVDNLKDGTKFANLVD
LDIADYCDKEDFIASIIAGDEFGDIDAVFHEGACSATTEWDGKIMHNNYEYSKELLH
YCLDREIPFFYASSAATYGDTKVFREEREFERGPLNVYGYKFILFDQYVRHILFBAKS
VCGFRYFNVYGPRENHKGSWASVAFHLNNQILKGENPKLFAGSEHFRRDFVYVGDVAA
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EAAALGGAIQAMWANGEGELEFLCETFIHLDENSKAYPNLSQVKNYQNAYERYLTHLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="thioredoxin, putative"
/protein_id="AAC22769.1"
/db_xref="GI:1574669"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
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/protein_id="AAC22768.1"
/db_xref="GI:1574668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity; putative"
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                                                                                                         McDonald, L., Artiach, P.,
                                      sequence
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                                      of Treponema pallidum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                     Bowman, C.,
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                                      the syphilis
                                                                                                         Cotton, M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-MAR-1998) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 281 (5375), 375-388 (1998)
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9665876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MELQKKFTALAQSQVELEVVVAREDAQRHYQRFVBEYLERARLP
GFRKGKVPLAVLERKYGSAIRQDAAAALMEKALEGFAQASQDSQPLPISRPSLKKKP
VPDPDEDFSFAVIYDVFPSVELRNTSGFSLSVPTVSVTEEDVSRELTRQDERNALTVD
KGADSCAEVGDIATVDYHEVDDSGAVRPGTERAGVVFTLGVEEGFFALGQDILGWKLG
QRCLFAKRAGMLKDEAAQVRVTLKALKQRQLPSLDDELAQDVSDAFRTLDDLTRSVRQ
/trānslation="mrerminlvpyvieQsGggersyDifsrllkDriifvDgeItDA
VablvVaQLLFLeSQNeDKDISLYINSPGGAVTAGLAVYDTMQHICPEVQTICLGQAS
SMAAVLLAGGAPGKRFALESSRVMHIQPWGGVQQQASDVCIQAQEILRLKTLTIAYFA
LHTGQSEEQVREDMERDFFLSAEQACSYGIVDTVMKRRKHAQV"
                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:L42023 SP:P43867 PID:1005637
PID:1220799 PID:1204962 percent identity: 60.42;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLAEALEAALHEYKRRQLLRILVRENPFSLPESLVVGEMESRWALVMRQFGVSLSGTP
QNKLQFFQQWRPEVEEHLKQRVIVELLLKQEQVSVSAEEIETEYVRIASKTGSKEERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REYYAGEEKRRALCEGIRERKLCQKLLGRCVTECGPEQSLTDFLQEQSRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="trigger factor (tig)"
/protein_id="AAC65494.1"
/db_xref="GI:3322798"
                                                                                                                              protein_id="AAC65495.1"
/db_xref="GI:3322799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                          product="ATP-dependent Clp
                                                                                                                                                                                                                                                                             codon_start=1/
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to GB:AE000783 percent identity: 25.17; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="TP0506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="tRNA-Leu-4"
'product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:160'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="TP0507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="TP0507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="TP0506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="codon recognized: GGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="tRNA-Gly-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="tRNA-Gly-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="codon recognized: AAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="tRNA-Lys-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="tRNA-Lys-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .26849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="codon recognized: CUA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26849)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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YDSAYRIFQDEMCFALGLRPPEVETLIHGYLEKAKENPVVSGTVDVPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="TP0511"
6456. .7082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDTTTDASCPCDTPRAGFRRVKPVVFSSVYPVDTDECEQLREALERLALNDASISWER
DSSLALGHGFRCGFLGLLHLEVVQQRLEREFNQTFTAPQVQYVVFLKTGQRIVCDN
PAHYDLEQEIAQVHEPYIRATITTPTBVLGAVQTLEREKAYQTAVNYLDQKRVELVY
PAHYPLEQEIAQVHEPYIRATITSVTEVIGAVQTLEKKAYQTAVNYLDQKRVELVY
EMPLABILFGFVDRLKSISHGYASFDYELIESKLTDLVKVDILINGKPVDALAQLCYR
PHARRAQAVCAKLKEBISRQQFKIAIQGSIGGQIISRETVSPFRKDVLAKCYGGDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="GTP-binding membrane protein (lepA)"
/protein id="AAC65498.1"
/db_xref="GI:3322802"
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/translation="MRAACVURVENFCIVAHIDHGKSTLADELIERTRAVEERLOHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:L18867 SP:P33138 GB:Z23278 PID:347729 PID:388977 percent identity: 56.78; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALLVVDATQGVESQTISNLYLVLEHNLEIIPVINKIDLPTADVPRVLQQVEHDLGLD
PASSVLISAKTGENVDALFDAIITRIPPPQGSGTAALQALVFDCHYDQYRGVVVHIRV
FEGQVTSGMVIRFMSNGAEYRVEETGVFVFNLIAREALCAGDVGYLSANVKTVSDVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mesligkrvidfklpayvggkftevsnasikgswavfmfypadf
tfvCpteladlarvypsfvEigckvysvstdseyvhkawadatdtiknlpyemisdka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative"
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3849. .4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITKKVVTQEEKASVRLVSERTA"
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ALFALDDVRLVFDEDALDA I AQQA I DQKTGARGLRS I VERLMLDAMFEAPSLKGKKEL
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IDSVLIEKSNVLLIGPTGSGKTLLAKTLSQKMKVPFAIADATTLTEAGYVGEDVENIL
LKLVQNANGDVALAERGIIFIDEIDKISRKSENVSITRDVSGEGVQQALLKIIEGTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity;
                                                                                                                                                                                                                                                                                                            6456. .7082
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/note="similar to GP:1881322 percent identity: 31.79;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKRKLLEKQKEGKKRMKMVGDVEIPQTAFLSVLKEASDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4596. .6413)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKLAGFFGVLLPDTWHALRGTFVVDPEGLVKAFEVHDMGIGRDADELLRKVQSAQFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl table=11
/producT="alkyl hydroperoxide reductase (ahpC)"
/protein id="AAC65497.1"
/db_xref="GI:3322801"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to identity: 48.92; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /producT="ATP-dependent Clp protease subunit X (clpX)"
/protein_id="AAC65496.1"
/db_xref="GI:3322800"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transI_table=11
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/gene="TP0509"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="TP0508"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to GB:AE000783 percent identity: 59.57; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="TP0510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MLRSKGDLVLGCSFCGKKEDERRRIVTGHGVSICNYCVERCAE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                             table=11
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Search completed: January 30, 2004, 10:14:24 Job time: 2286 secs
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                    5442
                                                                                                                                 424 CCTCAACGACGCAAGTATTTC 444
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                                                                                                                                                                                                                           Similarity
                                                                                                    CCTCAACGACGCAAGTATTTC
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                           similarity; putative"

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/trans1_table=11
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/product="K+ transport protein (trkA)"
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HYAHANCRESSRCIFGTBLISADKEAMRAVVSTVBCAAISDVIPLKNARYEIARFPIA
KGSGLDGITLSDMRRLVKISFVAVAFEVRGRSVIPSGETMLASGMRLSVLCAPEHMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mrrggacvokkeylpltsropgvcllseilvralearsfflvvv
Tvpagevayaesqvacdsrlsaffesrtrpvllyvpgattrsasvragldamathapdv
Tvphgerpfysvallhsvlbatcrygarvierghytpkgvadgsiethlirsrp
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Leqrasepaltrgisvlpcteegalryglgtdmhalcagrplliagihlpskkcaqgh
Sdadvlahasidallgaaglgdigtffpscdgrwkdahscallrhtwqlvraacwrlv
Nldavvcleqpalhpfreamraslaqaldthvtrvfvkaktaerlgpvgsgaavtaqv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:X72382 SP:Q08113 PID:313163 pe
identity: 36.31; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                      FYELAGFKIHPVKKIALIGMSAVGTLVAQDVAEKCKPHFFSSAFSLSPRERASLVLVD
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/gene="TP0512"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="similar to SP:P23868 GB:X52114 PID:43137 PID:443993
PID:606224 percent identity: 23.86; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAC65500"
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transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="TP0513"
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Pred. No.
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                          Pred. No.
                                                                                                 Score
                                                                                                                                                    d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants
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P-PSDB; ABB81626.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 39; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EXEL-) EXELIXIS PLANT SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
                              GAAGAAGATGAAGAGGTTGTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
                                                                                  TCGATGGACAACGTAGATCCATGGTGGATAAATTTACTGGAAAATTGCAATGACGATATT
                                                                                                                                                                                                 AACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATT
                                                                                                                                                                                                                                                                                                                                                         CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                             AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  825 BP; 309
               GAAGAAGATGAAGATTTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
                                                                   TCGATGGACGAACGTAGATCCATGGTGGATAAATTTACTGGAAAATTGCAATGACGATATT
                                                                                                                        AMACCTCAACGACGCAAGTATTTCTCAAGCACAATGAAGAATGTTACAAAACAATAATGTA
                                                                                                                                                                                                                                 GTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATTAGTACTAAGATTGAAATTATA
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                                                                                                                                                                                                                                                                                                                                                                                               AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 825; D
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 226 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Length
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RESULT 2
ABQ73048
ID ABQ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants -
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conners
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomato anthocyanin 1 (ANT1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour;
AACAATAAGTGTGGAGAAATTAGTACTAAGATTGAAATTATAAAACCTCAACGACGCAAG
                                                                                 TGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATT
                                                                                                            TGGAACACTAATCTTCTAAGGAAGTTAAAATACTACTACTAAAATTGTTCCTCGCGAAAAGATT
                                                                                                                                                                                                               AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGATTTTTCTGCTGAAATTGACTTATGGAATCTACTTGATTAA 825
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                                                                                                                                                                              AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 46-47; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mathews HV,
                                                                                                                                                                                                                                                                         68.7%; So ilarity 100.0%; I Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                          364 A; 138 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic fragment SEQ ID NO: 4.
                                                                                                                                                                                                                                                                         Score 567; DB 24; ]
Pred. No. 3.6e-273;
O; Mismatches O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                          201 G; 309 T;
                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents an example from the present
                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                       Length 1012;
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     RESULT 3
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16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; microbial disease resistance; herbicide resistance; see
     Pilgrim
                                                                                                                                                                                                                            (CREE/)
(DUBE/)
(HEAR/)
(JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
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                                                                                                                                                     (KEDD/)
(ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                         (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001; 2001WO-US26189
                                                                                                                                 (REUB/
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                                                                                                                 ADAM L.
) RATCLIFF O.
                                                                                                                                                                                             HEARD J.
JIANG C.
KEDDIE J.
                                                                                             REUBER J L.
RIECHMANN J )
       Σ
                                                                                 YU G.
                                                                                                                                                                                                                                                                       CREELMAN R.
DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                     MENDEL BIOTECHNOLOGY INC.
                                                       PINEDA O.
                                                                                                                                                                                                                                                                                                                         PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGTCATGAAAATTGGGGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a transcription factor
       Creelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth
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          Dubell
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          Heard J,
       Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 senescence.
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seed yield;
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          Keddie J;
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985 798 925 738 865 678 805 618 745 558 589 498 625

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AAAO1109/c

ID AAAO1109;

XX

AC AAAO1109;

XX

DT 19-MAY-2000 (first entry)

XX

DT 19-MAY-2000 cancer cell lir

XX

Human colon cancer; tumous

KW Human; colon cancer; tumous

KW probe; detection; cancerous

KW breast cancer; oestrogen ri

KW oestrogen receptor-negativ

XX

PM W09958675-A2.

XX

PD 18-NOV-1999.

XX

PR 13-MAY-1998; 99WO-US1060

XX

PR 11-MAY-1998; 98US-008542

PR 11-MAY-1998; 98US-008542
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compression approximation approximation of known plant
compression of the plant of the plant
compression approximation sequence information selected from one of
compression and the sequence solven in the specification. The isolated or
complete trait, the method comprising selecting a plant having a
complete trait, the method comprising selecting a polymucleotide that
compression and selecting a polymucleotide that
composition or an antisense nucleic acid, inserting the
colymucleotide or antisense nucleic acid into an expression vector,
composition of a plant or a cell of a plant to overexpress
composition of a plant or a cell of a plant to overexpress
composition of agriculturally useful proteins or metabolic chemicals,
composition of agr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 523-525; 941pp; English
                                                                                                                                                                                                                                                                                                                           breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1300 BP; 392 A; 210 C; 350 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated or recombinant polynucleotide used to produce a transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer cell line polynucleotide sequence SEQ ID NO:1100.
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                                                                                                                                                                                                                                                                                                                                                                                colon cancer; tumour; diagnosis; gene expression product; detection; cancerous state; metastasis; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCAACAGATGGTCACTTATTGC 445
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           98US-0085426.
98US-0085537.
                                                                                                    99WO-US10602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                              cellular fucosylation; glycoconjugate fucosylation; transplant rejurititis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 300 BP; 128 A; 44 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 445; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide library used to determine cancerous states of mammalian
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                                                                                                                                                                                                                                                                                                                  Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #2452
                                                                                                                                                                                                                                                                                                                                                          10-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX20395 standard; cDNA;
                                                            15-AUG-2002.
                                                                                                                                                                              antiasthmatic;
                                                                                                   US2002110548-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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98US-0105234.
98US-0105877.
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Randazzo F, Kennedy GC,
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                           GM4,6D; gene; ss; inflammation; e fucosylation; transplant reje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
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Stache-Crain B;
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                                                                                                                                                                                                                                                           rejection;
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11-JUN-2001; 2001US-0878574.

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RESULT 6
AAA02459/c
ID AAA02459;
XX AAA02459;
AC AAA02459;
XY 19-MAY-200
XX Human colc
XX Human; col
KW probe; det
KW probe; det
KW probe; det
KW oestrogen
XX Homo sapic
XX Homo sapic
XX Homo sapic
XX Homo sapic
XX PN WO9958675;
XX PN HOMO SAPIC
XX PN HOMO SAPI
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Best Local S
Matches 21
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03-DEC-1997;
09-SEP-1998;
14-JUN-1999;
  14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the level of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding human GM4,6D peptides of the invention.
                                                                                                                                                                                                                                                                                                                                    probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000
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                                                                                                                  13-MAY-1999;
                                                                                                                                                                         18-NOV-1999.
                                                                                                                                                                                                                              WO9958675-A2
                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a composition comprising a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGTGAAAAACTATTGGAAC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 BP; 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer cell line polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; tumour; diagnosis; gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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97US-0984246.
98US-0149674.
99US-0333177.
  98US-0085426.
98US-0085537.
98US-0085696.
                                                                                                                  99WO-US10602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 59 C; 101 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:2450
                                                                                                                                                                                                                                                                                                                                                                                                                         product;
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RESULT 7
AAT42063/c
ID XXX ACC XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                     07-JUN-1995;
21-APR-1995;
07-JUN-1995;
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                    expression modulating fragment; regulation; organism; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                        Genome; bacterium; Haemophilus influenzae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae complete genome sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide library cells -
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27-OCT-1998;
                                                                                                                                                                                                                                                                                 Haemophilus
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(HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAAGTGGATCTCATTTTGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765 BP; 298 A; 123 C; 136 G; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer, lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 982; 1097pp;
                                                                                                                                                                                                                                                                                   influenzae
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                     95US-0487429.
95US-0426787.
95US-0476102.
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98US-0105877.
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Randazzo F, Kennedy GC, I
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Stac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            gene expression;
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Pot D, Kassam A;
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Matches
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                                                                                                                                                                                    24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae Rd genome medium - useful for identifying fragments by homology searching
                                                                                                                                               (SCRI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 77.2-77.1091; 1291pp; English.
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                                                  Identifying a stress condition to which a plant cell has been and producing plants with increased tolerance to these abiotic
                                                                                                                    Harper JF,
                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-US26685
                                                                                                                                                                                                                                                                  28-FEB-2002
                                                                                                                                                                                                                                                                                            WO200216655-A2
                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana;
                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana stress
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             Claim 144;
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SYNGENTA PARTICIPATIONS AG.
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21; Conservative (
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                                                                                                                    Kreps J,
                                                                                                                                                                                    ; 2000US-227866P.
; 2001US-264647P.
; 2001US-300111P.
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                              plant; gene; stress; transgenic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 21;
100.0%; Pred. No.
                                                                                                                    Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       В₽
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                                                                                                                                                                                                                                                                                                                                                                       regulated gene SEQ ID NO 121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
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                                                                           06-MAY-1999;
07-MAY-1999;
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06-MAY-1999;
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                        11-MAY-1999;
14-MAY-1999;
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05-AUG-1999 05-AUG-1999 05-AUG-1999 05-AUG-1999 05-AUG-1999 05-O1477303 06-AUG-1999 07-O1477303 06-AUG-1999 07-O1477303 07-AUG-1999 07-O14871 11-AUG-1999 1908-O14871 11-AUG-1999 1908-O148865 17-AUG-1999 1908-O149368 17-AUG-1999 1908-O149722 20-AUG-1999 23-AUG-1999 2908-O149722 27-AUG-1999 2908-O149723 27-AUG-1999 2908-O150864 27-AUG-1999 2908-O150864 27-AUG-1999 2908-O150866 27-AUG-1999 2908-O15086	27-JUL-1999; 99US-01: 27-JUL-1999; 99US-01: 27-JUL-1999; 99US-01: 28-JUL-1999; 99US-01: 02-AUG-1999; 99US-01: 02-AUG-1999; 99US-01: 02-AUG-1999; 99US-01: 03-AUG-1999; 99US-01: 04-AUG-1999; 99US-01: 04-AUG-1999; 99US-01:

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26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                          The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ
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                                                                                           Sequence 684707 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
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AAK62944 standard;

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AAK62944;

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Note: The sequence data for this patent did not form part

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Note: The sequences.
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                                                                                                                                                                                                                                                                                                                                                                        New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
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                                                                                                                                                of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaser P;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria; food contamination; mutational analysis;
                                                                       100.0%;
                                                                                                                    941651 A; 568176 C; 559189 G; 942192 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECH
                                                                                        2.48;
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                                                                         Score 20; DB 24;
Pred. No. 9.1;
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                                                            Mismatches
                                                            0
                                                                                       Length 3011208;
                                                                                                                                                                                                                                                                                                                                                                                         polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                         for detection,
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                                                            Gaps
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W0200157182- 09-AUG-2001. 17-JAN-2000. 04-FEB-2000. 16-MAR-2000. 17-MAR-2000. 11-MAR-2000. 11-MAR-2000. 11-MAR-2000. 11-MAR-2000. 11-MAR-2000. 11-MAR-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-JUL-2000. 11-AUG-2000. 11-SEP-2000. 10-SEP-2000. 10-SEP-2000. 00-SEP-2000. 00-SEP-2000. 00-SEP-2000. 00-SEP-2000. 00-SEP-2000. 00-SEP-2000. 11-SEP-2000. 01-SEP-2000.	Human immune/h Human; immune; cytostatic; ge
A2. 2001WO-US01354. 2000US-019065. 2000US-0184664. 2000US-0184664. 2000US-0199123. 2000US-0199123. 2000US-0199123. 2000US-0209467. 2000US-0209467. 2000US-0216649. 2000US-0216649. 2000US-0216649. 2000US-0216649. 2000US-0225214. 2000US-0225214. 2000US-0225266. 2000US-0225266. 2000US-0225266. 2000US-0225267. 2000US-0235447. 2000US-0233144. 2000US-0233144. 2000US-0233144. 2000US-0233144. 2000US-0233144. 2000US-023329. 2000US-023329. 2000US-023329. 2000US-023329. 2000US-023329.	aematopoietic haematopoieti ne therapy; va
	ntigen encoding; immune/haematc
	CDNA SEQ ID NO:8 poietic antigen;
	:8004. 1; cancer;
%	PR PR PR PR
26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-CCT-2000 02-CCT-2000 03-CCT-2000 03-CCT-2000 04-NOV-2000 06-NOV-2000 08-NOV-2000 08-NOV	- 4 ES
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RESULT 13
AAS22921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
03-FEB-2000;
20-JUN-2000;
19-JUL-2000;
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08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                 Bone marrow; diagnostic; therapeutic; gene therapy; antigenic; haematopoiesis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 464 BP; 155 A; 103 C; 112 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 8004; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                            05-FEB-2001;
                                                                                            09-AUG-2001
                                                                                                                        WO200157187-A2
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                      severe
                                                                                                                                                                                                                                                                DNA encoding
                                                                                                                                                                                                                                                                                                                                                          AAS22921 standard; DNA; 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-483426/52.
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                                                                                                                                                                                     combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATGGACTGATGAAGAA 304
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; 2000US-0496914.
; 2000US-0598075.
; 2000US-0620325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                              2001WO-US03782.
                                                                                                                                                                                                                                                                novel bone marrow polypeptide #15
                                                                                                                                                                                                                                                                                              (first entry)
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Pred. No.
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cc acids may be used to produce the polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. CC The nucleic acid and its complementary sequences may also be used as DNA CC probes in diagnostic assays to detect and quantitate the presence of CC similar nucleic acid sequences in samples, and therefore which patients CC may be in need of restorative therapy. The proteins may also be used as CC antigens in the production of antibodies against bone marrow proteins CC and in assays to identify modulators of their expression and activity. The anti-bone marrow protein antibodies and antagonists may also be used CC odown regulate expression and activity. The antibodies may also be used CC as diagnostic agents for detecting the presence of the protein suggested to regulate expression and activity. The antibodies may also be used CC may be used to regulate haematopoiesis activity, and consequently in the treatment of myeloid or lymph cell disorders; in tissue regeneration, cc such as wound healing; as a nutritional supplement; and in treatment of immune disorders such as severe combined immunodeficiency (SCID).
                                                                                                                                                                                                                                                                                                                                                                                                                                       inappropriate bone marrow polypeptide expression. For example, to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of the polypeptides by expressing inactive proteins or to supplement the patient's own production of the polypeptide. Additionally, the nucleic patient's own production of the polypeptide. Additionally, the
Sequence 737 BP; 232 A; 112 C; 182 G; 191 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS22907-AAS23099 represent nucleic acids encoding novel bone marrow polypeptides. The nucleic acids and corresponding proteins may be used in the prevention, diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 162; 392pp; English.
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  20 other;
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Ś Matches Query Match Local 617 l Similarity
19; Conserv TTGTAATTAATTATGAAAA 635 Conservative 100.0%; 2.3%; <u>,</u> Score 19; Pred. No. Mismatches 33; 22; Length 737; 0, 0 Gaps

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TTGTAATTAATTATGAAAA 609

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RESULT 14
AAA70171/c
ID AAA70171;

XX
AC AAA70171;

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C AAA70171;

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AC AAA70171;

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AC AAA70171;

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AC AAA70171;

XX
AC AAA70171;

XX
C Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:304.

XX
AC Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; XX
AC AAA70171;

XX
AC Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; XX
AC Plasmodium falciparum.

XX
AC Plasmodium falciparum.

XX
BN
WO200025728-A2.

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DD
11-MAY-2000.

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D5-NOV-1999; 99WO-US26796.

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O5-NOV-1998; 98US-0107131.
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ID AADOS784
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XX Trans
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; biochemical characteristic; controlling structural characteristic; developmental characteristic; gene agricultural biotechnology; plant trait modification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF/)
(CARU/)
(GARD/)
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                                                                                             WO200136597-A1
                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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CARUCCI D.
GARDNER M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Suc. 100.0%; Pred. No. 1
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                                                                                                                                                                                 "Transcription factor, G1324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 T; 0 other;
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25-MAY-2001.

Search completed: January 30, 2004, 09:36:34 Job time : 282 secs

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Best Local
                                                                                                                                                         soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas, Transcription factors are key controlling elements of biological pathways and altering expression levels of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits. Transcription factor cDNA is useful in
                                                                                                                                                                                                                                                                                                                             The present sequence is Arabidopsis thaliana transcription factor, G1324 cDNA. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be used to alter the structure and developmental characteristics of plants such as alter the structure and developmental characteristics of plants such as
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn, potato and cotton plants - \,
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Pilgrim M, Pineda O,
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                                                                                                                                                  gene therapy
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                                                                          Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Fax: 580 221 7380
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days. Cells were induced six days after subculture"
/clone_lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 an 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
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                    /organism="Medicago truncatula"
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  185
                                            175 TATCTAAGGCCACATATCAAGAGAGGTGACTTTG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
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Email: http://www.genome.clemson.edu/orders/index.html
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BE462229
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EST324493 tomato flower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from tomato flower tissue,
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TATCTAAGGCCACATATCAAGAGAGGTGACTTTG 218
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                                                                                      Conservative
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                                                                                                                                                                                               /tissue_type="flower"
/dev_stage="0-3mm buds"
/dev_stage="0-3mm buds"
/clone_lib="comato flower buds 0-3 mm, Cornell University"
/clone_stape="comato flower buds 0-3 mm, Cornell University"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
sze-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture" /clone_lib="Elicited cell culture" /note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 ar 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation." a 122 c 128 g 183 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4081"
/clone="cTOA12C3"
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3.4e-07;
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EST320028 tomato radicle, 5 d post-imbibition, Cornell University Coperation esculentum cDNA clone cLEZ18K18 5', mRNA sequence
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                BE462282 490 bp mRNA linear EST 18-EST324546 tomato flower buds 0-3 mm, Cornell University Lycopersicon esculentum cDNA clone cTOA12C2, mRNA sequence.
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100 Jordan Hall, Clemson,
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BE462282
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                                                                  Contact: CUGI
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79 c 91 g 119 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="radicle"
/dev_stage="seedlings 5 days post-imbibition"
/cione_lib="tomato radicle, 5 d post-imbibiti
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                             Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M276687e
TIGR sequence name: MTFCE77TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S Holt,I.E. and Fraser,C.M.
ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
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EST456718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula (barrel medic)
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651 649 5058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="0-3mm buds"
/clone lib="tomato flower buds 0-3 mm, Cornell University"
/clone lib="tomato flower buds 0-3 mm, Cornell University"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
size-separated while remaining frozen."
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
                                                               trifolii"
                                                                                                                        /mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                            Location/Qualifiers
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DSIL Medicago truncatula
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/clone="cTOA12C2"
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                                                                                      /tissue
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                                                                                  type="leaves infected with Colletotrichum
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Pred. No.
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Bowman,C.L.,
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1e-06;
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CDNA
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Craven, M.B.,
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BF635572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GATTGAGGTGGCTGAATTATCTAAGGCC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; eulicotyledons; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Fowned Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF635572 367 bp mRNA linear
NF104H01DT1F1014 Drought Medicago truncatula cDNA
                                                                                                                                                                                                                                                                                                                                           Email: gdmay@noble.org
Insert Length: 367 Std Error: 0.0
Plate: 104 row: H column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="DSIL"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
74 a 32 c 66 g 73 t
                                                                                               142 a
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                                                                                               timepoints.
                                                                                                                                  /note="Vector: Lambda Zap; Contains a mixture of enti
plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                   /organism="Medicago truncatula"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                              /db_xref="taxon:3880"
/clone="NF104H01DT"
                                                                                                                                                                        clone
                                                                                                                                                                                            dev_stage="Pooled timepoints"
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                 3.3%;
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Score 27; DB Pred. No. 0.0 0; Mismatches
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Pred. No.
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clone NF104H01DT
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RESULT 9
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AW980341
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               DEFINITION
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                                                                                                                                                                                                                                                                          151 AGTTGTAGATTGAGGTGGCTGAATTAT 177
       BF006562 526 bp
EST435060 DSLC Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                    27;
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: vance004@maroon.tc.umn.edu University of Minnesota name:M256175e
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Contact: Carroll P. Vance
Contact of Agronomy and Plant Genetics
Department of Minnesota
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     truncatula
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Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW980341 526 bp
EST391494 GVN Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR sequence name:MTCBH30TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
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                                                                                                                                                                                                                                    AGTTGTAGATTGAGGTGGCTGAATTAT 409
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651-649-5058
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,I.E. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=Tvector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
75 c 108 g 160 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E._coli strain XIOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="genotype_A17"
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Bowman,C.L.,
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mRNA linear EST 06-OCT-CDNA clone pDSLC-42B13, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
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                                                                                                                                              sequence.
BE124179
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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ESTs from Medicago truncatula leaves and cotyledons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M275600e TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Plant Pathology University of Minnesota
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                                                          Medicago truncatula (barrel
Medicago truncatula
                                                                                                                                                                                                          BE124179
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Fax: 651 649 5058
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/clone lib="DSIC"
/note="Webtar prepared from polyA+ enriched RNA from the KhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of cotyledons of five days old plants and leaves of two weeks old plants. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaves and cotyledons"
/dev_stage="mixture of cotyledons from fiv
plants and leaves obtained from two weeks
/lab host="E. coli strain SOLR"
/clone_lib="DSLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in SOLR cells."
98 c . 110 g 127 t
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/mol_type="mRNA"
/cultivar="genotype_A17"
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Pred. No. 0.0067;
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eks old plants"
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RESULT 11
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TITLE
JOURNAL
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                                                                                                                                                                                                                      sequence.
BG588067
BG588067.1
EST.
                                                                                                                 Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; Pabaceae; Papilionoideae; Trifolieae;
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EST489876 MHRP- Medicago
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Minnesota sequence name:M262137e
TIGR sequence name:MTFBH30TKB
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Tel: 612 625 1243
Fax: 651 649 5058
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ESTs from phosphate-starved roots of Medicago truncatula, 2001
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Plant Pathology University of Minnesota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                         Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTTGTAGATTGAGGTGGCTGAATTAT 177
                                                                              (bases 1 to 585)
                                     Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="DSIL"
//clone lib="DSIL"
//note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2:
//note="Vector: preserved from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the Uni-ZAP XR vector from directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chrysie.tamu.edu/medicago
imer: SKmod (CTA gAA CTA gtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E__coli strain XLOLR"
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/clone="pDSIL-13E12"
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100.0%; Pr
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                                                                                                                                                                                                                                                                                               585 bp mRNA linear EST 12-APR-20 truncatula cDNA clone pMHRP-41C11, mRNA
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27; Conserv
                      Tel: 706-542-4457
Fax: 706-542-4412
                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                          Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                           BG647939
                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
      Email: hahn@ccrc.uga.edu
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COMMENT
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Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Vai
Utterback, T., Cho, J. and Fraser, C.M.
ESTS from roots of Medicago truncatula treated with
Cliggalacturonides of DP 6-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG647939 618 bp mRNA linear EST 24
EST509558 HOGA Medicago truncatula cDNA clone pHOGA-18G24
University of Georgia
220 Riverbend Road, Athens,
                                                                                              Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula (barrel medic)
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EST.
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Seq primer: SKmod (CTA c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Samuel Roberts Noble Foundation: N266740e TIGR sequence name: MTHAI18TKB More information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Biology Division
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTGTAGATTGAGGTGGCTGAATTAT 177
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/clone lib=MmRP-
/clone 
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/mol_type="mRNA"
/cultivar="A17"
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| lab_host="XLOLR"
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Pred. No. 0.0069;
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                                                                                                                                         available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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EST508845 HOGA Medicago truncatula cDNA clone pHOGA-16E11 5' end,
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Seg primer: SI
                                                                                                                                                                                                                                                                                                     Complex Carbohydrate Research Center University of Georgia
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                                                                                                                                                                                                   G390832e TIGR sequence name: MTMBW30TK More information
                                                                                                                                                                                                                      Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                                                                                                220 Riverbend Road,
                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula (barrel medic)
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706-542-4412
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118 c 117 g 172 t
                                                                                                                                                                                                                                                                                                                                              Michael G. Hahn
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/tissue_type="3 day old seedling roots"
/tissue_type="3 hours after treatment in the dark at
/dev_stage="24 hours after treatment in the dark at
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="XIOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The was directionally ligated into the Unizap XR vector fr
/db_xref="taxon:3880"
/clone="pHOGA-16E11"
/tissue_type="3 day old seedling roots"
                                                            /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
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/mol_type="mRNA"
/cultivar="A17"
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BU830456
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BU876538 308 bp mRNA 1
V021H11 Populus flower cDNA library Populus
trichocarpa cDNA 5 prime, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rupali.bhalerao@plantphys.umu.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +46 90 786 5279 Fax: +46 90 786 6676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: BHALERAO RUPALI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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The poplar tree transcriptome:
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//clone lib="HOGA"
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="24 hours after treatment in the dark at 26 with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                    /organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="apical shoot"
/clone_lib="Populus apical shoot cDNA library"
147 c 183 g 181 t
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Pred. No.
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Pred. No.
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0.0072;
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Populus tremula x Populus
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                     balsamifera
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AUTHORS
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source
Search completed: January 30, 2004, 10:47:17 Job time : 2028 secs
                                                                                             밁
                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                Query Match 3.0%; Score 25; DB 13; Best Local Similarity 100.0%; Pred. No. 0.066; Matches 25; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: BHALERAO RUPALI R.
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6576
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
Tel: -308
                                                                                                                    590 ATGACGATATTGAAGAAGATGAAGA 614
                                                                                          139 ATGACGATATTGAAGAAGATGAAGA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Populus balsamifera subsp. trichocarpa
Populus balsamifera subsp. trichocarpa
Populus balsamifera subsp. trichocarpa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malphyhiales; Salicaceae; Populus.

1 (bases 1 to 308)
Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Onpublished
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BU876538.1 GI:24068062
                                                                                                                                                                                                                                                                                              /organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub species="trichocarpa"
/db_xref="traxon:3694"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
75 c 59 g 86 t
                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                             Length 308;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Length	BB	ID	Description
ם	1477	100.0	274	23	ABB81626	Tomato anthocyanin
2	542.5	36.7	246	22	AAE01932	Arabidopsis thalia
ω	542.5	36.7	246	23	AAU93177	Arabidopsis transc
4	538	36.4	248	23	AAU75734	A. thaliana Produc
₅	535	36.2	249	22	AAB68356	Amino acid sequenc
6	532.5	36.1	249	22	AAE01916	Arabidopsis thalia
7	532.5	36.1	249	23	AAU92969	Arabidopsis transc
œ	532.5	36.1	249	24	AAE30046	Arabidopsis thalia
9	527	35.7	249	23	AAU75735	A. thaliana Produc

45	44	43	42	41	40	39	38	37	36	35	3 4	ω	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	
374	374	374	375	375	377	377.5	77.	377.5	77.	377.5	79.	385	87.	387.5	88	393	396.5	397	399.5	400	401	402.5	403	403	408	408	408	408	415	420	422	510	518.5	518.5	524	
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371	371	273	280	280	268	274	274	236	236	236	258	246	255	253	153	120	302	342	176	148	203	226	257	246	278	269	269	258	205	391	302	211	209	209	212	
23	22	23	22	21	23	22	21	22	21	21	23	23	21	23	21	23	23	23	21	21	23	22	21	21	21	22	21	21	21	21	22	22	23	22	23	
AAU92995	AAE01913	ABJ10416	AAB68353	AAG31515	ABJ10423	AAE02485	AAG31297	AAB67842	AAG49909	AAG08529	ABJ10408	ABJ10422	AAB33306	ABJ10420	AAB33239	ABJ10409	ABJ10412	AAU93088	AAB33283	AAB33044	AAU93131	AAB82482	AAG30441	AAG30442	AAG29947	AAE02486	AAG29948	4	AAB33293	AAB33304	AAB82483	AAB68355	AAU93176	93	AAU93155	
	Arabidopsis thalia	Myb-related transc	Amino acid sequenc	Arabidopsis thalia	Myb-related transc	Arabidopsis thalia	Arabidopsis thalia	Amino acid sequenc	Arabidopsis thalia		Myb-related transc	Myb-related transc	Pinus radiata tran	Q.	ഥ	Myb-related transc	Myb-related transc		Pinus radiata tran		Arabidopsis transc	Ø	Arabidopsis thalia					m	Eucalyptus grandis	Pinus radiata tran	Cotton transcripti	Amino acid sequenc	Arabidopsis transc		Arabidopsis transc	

ALIGNMENTS

PPP	X R R X	Y P S	Y PA	3	Y PF	X G X	B	\$ 8 X	\$ \$ \$	X D	X Z Z	X A X	RESULT 1 ABB81626 ID ABB8
New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g leaf color, flower color or fruit color in plants	WEI; 2002-557819/59. N-PSDB; ABQ73046.	Conners K, Mathews HV, Liu A;	(EXEL-) EXELIXIS PLANT SCI INC.	30-OCT-2000; 2000US-244685P.	29-OCT-2001; 2001WO-US50638.	18-ЛП-2002.	WO200255658-A2.	Lycopersicon esculentum.	Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour.	Tomato anthocyanin 1 (ANT1) protein SEQ ID NO:2.	24-SEP-2002 (first entry)	ABB81626;	LT 1 1626 ABB81626 standard; Protein; 274 AA.

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ARESULT 2
AREO1932
ID AREO
XX AREO
XX AFRA
DE AFRA
XX Tran
XW Stru
XW STru
XW STru
XW STru
XW Agri
XX Arab
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                                                                                                                                                                17-NOV-1999;
17-APR-2000;
22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE01932 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
(REUB/)
(CREE/)
(PILG/)
(RIEC/)
(JIAN/)
                                                                                                                                                                                                                                                                  14-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agricultural biotechnology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structural characteristic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana transcription factor homologue G2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE01932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colour or
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                                                                                                                                                                                                                                                                                                                                                                 WO200135727-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription factor; trait modification;
                                                                                                                     (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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PILGRIM M.
RIECHMANN J :
JIANG C.
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                                                                      CREELMAN R.
                                                                                               REUBER
                                                                                                                   MENDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 AA;
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2000US-0197899.
2000US-0227439.
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                                                                                               BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 9..110
                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Conserved_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1477; DB 23;
Pred. No. 1.9e-133;
w:amatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characteristic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seed characteristic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phremyl lipid content, to modify fatty acid and modify wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reuber :
Pineda (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics o plants, e.g. corn, potato and cotton plants -
                                                                                         Agriculture; metabolic chemical; environmental stress; microbial disease resistance; herbicide resistance; see fruit yield; growth rate; leaf senescence; flower senes
                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor G663. The transcription factors may modify traits associated with structural or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 114; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-335979/35.
N-PSDB; AAD05767.
                                             Arabidopsis thaliana.
                                                                                                                                                       Arabidopsis transcription factor #215
                                                                                                                                                                                                                                                      AAU93177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is homologue G2422 of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YUGG/) YU G.
(PINE/) PINEDA O.
(HEAR/) HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                            transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                             NKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSIT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLN----TTKIVP
                                                                                                                                                                                                                                                                                                                                 CNKDEQKDKLININLLDGDNMWWESLLE
                                                                                                                                                                                                                                                                                                                                                              C-KEIISEKQTPDASMDNVDPWWINLLE 194
                                                                                                                                                                                                                                                                                                                                                                                                                           REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Creelman
Heard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                          (first
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                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 542.5; DB
Pred. No. 1e-43;
26; Mismatches
                                                                                                                                                                                                                                                        246
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                                                                                              senescence.
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22-AUG-2000; 16-NOV-2000;

16-APR-2001;

28-FEB-2002

2001WO-US26189

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                                                                                                                                                                                                                 comprising a plurality was the sequence from a database comprising a plurality of known plant sequences comprising sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a concision of the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth crate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated with a plant trait as compared to a wild plant. Also include are a transgenic plant comprising the polynucleotides, a computer areadable medium having stored sequence information, and identifying a readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes exhibits ectopic expression or altered expression of one or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95%
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pilgrim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KEDD,
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                                                                                                                                         Local
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JIANG C.
KEDDIE J.
ADAM L.
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Ratcliff O,
                                                                                                                                         Similarity
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YU G.
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GKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMI-
                                                          GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLN----TTKIVP
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2000US-0713994.
2001US-0837944.
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                                                                                                                           26;
                                                                                                                                     Score 542.5; DB
Pred. No. 1e-43;
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                                                                                                                          Mismatches
                                                                                                                                                        DB 23;
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L, Yu G;
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Pineda O;
                                                                                                                                                          246;
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                                                                                                                        Gaps
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ARBSULT 4
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ANUT5734
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                                                                                                                                                                                             Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1

or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromosome

1. PAP1 and PAP2 are MYB-like transcription factors that regulate the

production of anthocyanin pigment. The nucleotide sequence of the

invention is useful for screening for PAP gene expression, it is also

cuseful for detecting promoter activity within a plant cell. The

culeotide sequence is also useful for screening for plant cell (e.g.,

A. thaliana) transformation. The transformed plant cells are then used

to produce transgenic plants with tissue-specific altered colour

expression. The nucleotide sequence is also useful for enhancing

accumulation of phenylpropanoid product in a plant. A transgenic

plant is useful for detecting a stress condition such as light

stress, water stress, pH stress, temperature stress, heavy metal

stress, pathogen attack or infection, wounding, nutrient deficiency,

herbivory, or abnormal hormone levels in a plant. PAP1 or PAP2

coversyression can also be useful for plant or PAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                     overexpression can also be useful in developing or enhancing d colouration in ornamental plants for commercial sales, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to the nucleotide and protein sequences of novel Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 26-27; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borevitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200200902-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sensitisation; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK14221.
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ROBERTS NOBLE FOUND INC SAMMUEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSIT 182
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                                                                                                                                                                              desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
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plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental colouration in ornamental plants for commercial sales, and ror sensitising plants to stress. Introduction of PAP1 or PAP2 sensitises

the A. thaliana PAP1

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ARBSULT 5
AAB68325
AAB68325
AC AAB6
XX AAB68
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DE Amin
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KW WYB
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Best Local (
                       The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB90. MYB polypeptides are useful for enhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a
                                                                                                                                                                                                                                   myloblastosis transcription a crop in a field -
                                                                                                                                                                                                                                                           Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resi
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-316365/33.
N-PSDB; AAF85191.
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23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant;
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  transgenic plant
                                                                                                                                                                              Claim 13; Fig 4; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  Tonelli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of MYB transcription factor AtMYB90.
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     with
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     enhanced stress
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Pred. No. 2.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                              resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 98
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                                                                                  for
                                                                                                                                                                                                                                                              Of.
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RESULT 6
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Best Local S
Matches 117
                                                                                                                                                                                                                                                                 17-NOV-1999;
17-APR-2000;
22-AUG-2000;
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                                                                                                     (MEND-)
(REUB/)
(CREE/)
(PILG/)
(RIEC/)
(RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; trait modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana transcription factor
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                                                              PINE/
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                                     PILGRIM M.
) RIECHMANN J
) JIANG C.
) YU G.
) PINEDA O.
) HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                           REUBER L.
CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                             MENDEL BIOTECHNOLOGY REUBER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDFEQDEVDLILKLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLKKLNTTKIVPREKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWSLFHGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SLLHEE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKDDEKDDFVN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNIISPPTTPVQKIGVFKPRPRSFSVNNGCSHLNGLPEVDLIPSCLGLKKNNVCENSITC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK 123
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                                                                                                                                                                                                                                                                 ; 99US-0166228.
; 2000US-0197899.
; 2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental characteristic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249
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Pred. No. 5.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seed characteristic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. stilbenes,
d phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy;
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Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in ger therapy. Therefore manipulating transcription factor levels in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is Arabidopsis thaliana transcription factor The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g. potato and cotton plants, when their expression level is altered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phrenyl lipid content, to modify fatty acid and modify
                                                                                                    plant; transcription
                                                                                                                                     microbial disease
                                                                                                                                                                                   Arabidopsis transcription
                                                                                                                                                                                                                      02-JUL-2002
                                                                                                                                                                                                                                                                                         AAU92969 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Specifically, they are used for modifying the nutritional content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                piants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pineda O,
                                   WO200215675-A1
                                                                  Arabidopsis thaliana
                                                                                                                  fruit yield; growth rate; leaf senescence; flower senescence
                                                                                                                                                     Agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-335979/35
                                                                                                                                                                                                                                                                                                                                                                                                           241 HENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 NNKCGEIST----KIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Page 70-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     great potential in agricultural biotechnology for modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD05751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVDPWWINLLEN---CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMOOGQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                          GEN-QEADAIVPEATTAEHGATLAFDVEQLWSLFD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                metabolic chemical; environmental stress;
sease resistance; herbicide resistance; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corn, potato and cotton plants -
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             NVCENSITCNKDDEKDDFV
                                                                                                  factor; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.1%; Score 532.5; DB 2 44.4%; Pred. No. 9.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133pp; English.
                                                                                                                                                                                   factor #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                           274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                     drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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밁 ş 밁 S

Matches Query Match

4 7

GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI

GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK

123 126 63 66

SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR

SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR

Local

Similarity

36.1%;

Conservative

34; Score Pred.

Mismatches 532.5; DB 2 No. 9.7e-43;

Indels Length 249;

43;

Gaps

DB 23;

Sequence

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CC readable medium having stored sequence information, and identifying a composition of the medium having stored sequence information, and identifying a common sequence from a database comprising a plurality of known plant common sequence comprising a plurality of known plant common sequences comprising sequence information. The isolated or combinant polymucleotide is used for producing a plant having a commodified trait, the method comprising selecting a plant having a commodified trait, the method comprising selecting a polymucleotide that concodes a polymeptide or an antisense nucleic acid, inserting the color polymucleotide or antisense nucleic acid into an expression vector, controducing the vector into a plant or a cell of a plant to overexpress the polymeptide or antisense nucleic acid, thereby producing a modified collant, and selecting for a modified trait (e.g. increased collant, and selecting for a modified trait (e.g. increased collant, and selecting for a modified trait (e.g. drought), microbial collars or metabolic chemicals, pest tolerance, nerbicide resistance, seed and fruit yield, growth collars or metabolic chemicals, and selecting for a modified trait (e.g. drought), microbial collars or metabolic chemicals, pest tolerance, herbicide resistance, seed and fruit yield, growth collars or metabolic chemicals.
                                                                                                                                                                                                                                                                                                                                                                            complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                              are a transgenic plant comprising the polynucleotides, a computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding an Arabidopsis thaliana transcription factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 40; Page 97-98; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated or recombinant polynucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2000;
16-NOV-2000;
                                                     specification). The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUBE/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KEDD/)
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.. Ratcliff (
                                                                         leaf and flower senescence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAM L.
RATCLIFF O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK65155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yd
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REUBER J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILGRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Creelman atcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-227439P.
; 2000US-0713994.
; 2001US-0837944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dubell AJ, Heard J,
uber JL, Riechmann JL,
                                                                         many other traits listed
                                                       one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang C,
TL, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  produce a transgenic
                                                       proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pineda 0;
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RESULT 8
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            a Mentha sp. or Taxus sp. terpenoid pathway gene where the terpenoid pathway gene encodes limonene synthase (LS) or taxadiene synthase (TDS). It is also useful for identifying one or more transcription factors that activate one or more genes of a biological pathway of a plant, fungi or animal cell, where the biological pathway can be a biochemical pathway such as biosynthetic pathways for soluble and insoluble carbohydrates, for amino acids and a response pathway to abiotic stress such as cold, freezing, drought, heat, nutrient deficiency, pH or biotic stress such as flowering, root development, a response pathway to environmental cues such as light intensity and light quality, circadian rhythm. Sequences
                                                                                                                                                                                                                              a polynucleotide which encodes a transcription factor for controlling the expression of one or more genes in a pathway. The method is useful for determining whether a member of a pool of test transcription factor polynucleotides encodes a biosynthetic pathway transcription factor or a primary metabolite pathway gene or a secondary metabolite pathway gene such as a terpenoid or alkaloid pathway gene transcription factor. It is also useful for determining whether a member of a pool of test encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; metabolite pathway; terpenoid; limonene synthase; alkaloid pathway gene; taxadiene synthase; biological pathway; freezing; abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress; infection; developmental pathway; flowering; root development; TDS; LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining whether one of several test transcription factor (TF) polynucleotides encodes pathway TF by determining expression from pathway gene promoter linked to reporter gene in a cell in present
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-018799/01.
N-PSDB; AAD47497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana G663 transcription factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                        present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
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are used
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                                                                                                                                                                                                                                                                                                                                                                      relates to a high-throughput method for identifying
                                                                                                                                                                                                                                                                                                                                                                                                             221pp; English.
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generate
transgenic
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAP2; production of anthocyanin pigment; MYB-like transcription factor; transgenic; plant; phenylpropanoid; stress; light stress; water stress; pH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. thaliana Production of anthocyanin pigment 2 (PAP2)
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                       Borevitz J,
                                                                                                                                     23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
                                                                                                                                                                                                                                                                                                                                                            misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                   (SALK )
(ROBE-)
                                                                                                                                                                                                      21-JUN-2001; 2001WO-US19734.
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                                                                                        SALK INST BIOLOGICAL
                                                                      ROBERTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVDPWWINLLEN---CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK
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215
                                                                      NOBLE
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                         Lamb
                                                                      FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "Encoded by
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No. 9.7e-43;
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WPI; 2002-164443/21.

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ARBSULF 10
AAU93155
ID AAU9315A
AC AAU93
XX AAU93
XX Arabi
XX Arabi
XX Agric
KW Agric
KW Fruick
KW Fruick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production of anthocyanin pigment. The nucleotide sequence of the cinvention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for plant cell (e.g., A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour carpetsion. The nucleotide sequence is also useful for enhancing carpension. The nucleotide sequence is also useful for enhancing carpension of phenylpropanoid product in a plant. A transgenic plant is useful for detecting a stress condition such as light carpens, water stress, pH stress, temperature stress, heavy metal carpens, pathogen attack or infection, wounding, nutrient deficiency, therefore, pathogen also be useful in a plant. PAP1 or PAP2 colouration in ornamental plants for commercial sales, and for colouration plants to stress. Introduction of PAP1 or PAP2 sensitises or lants to research more mightly to a stress of the parameters that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants to respond more quickly to a stress condition in ways that physiologically significant, as well as in ways of ornamental significance. The present sequence represents the A. thaliana PAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                                                            Agriculture; metabolic chemical; environmental stress; microbial disease resistance; herbicide resistance; secfruit yield; growth rate; leaf senescence; flower senes
                                                              plant; transcription
                                                                                                                                                                       Arabidopsis transcription factor #193
                                                                                                                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                                                  AAU93155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABK14222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAP1 and PAP2 are MYB-like transcription factors that regulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to the nucleotide and protein sequences of novel idopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 AP2. The genes for both PAP1 and PAP2 have been mapped to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 DEEEHCKEIISEKQTPDASMDNVDPWWINLLENCNDDIEEDEEVV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Page 28; 29pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                  standard; Protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              NKDDEKXDFVN----NLMNGDNMW---LENLLGENQEAXAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNIISPSTTPVQKIGVFKPRPRSFSVNNGCSHLNGLPXVDLIPSCLGLKKNNVCENSITC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNKCGEIST --- KIEIIKPQRRKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sis thaliana production of anthocyanin pigment (PAP) of the genes for both PAP1 and PAP2 have been mapped to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%;
                                                              factor; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 527; DB 23;
Pred. No. 3.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                  senescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----FSSTMKNVTNNNVIL 162
                                                                                                                             drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Arabidopsis thaliana

S В Ş

Query Match Best Local Matches

Similarity

35.5%;

DB 23; Length 212;

102; 7

Conservative

33; Mismatches Score 524; DB 2 Pred. No. 5e-42;

38;

Indels

38;

Gaps

SSLGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR

SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR

GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK---

114 63 66 ű Sequence

212

A

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CC associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant cC homologue sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a computer cC modified trait, the method comprising selecting a polynucleotide that cellocide is used for producing a plant having a composition of a polypup tide or an antisense nucleic acid, inserting the colynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress complete acid into an expression vector, and selecting for a modified trait (e.g. increased compant, and selecting for a modified trait (e.g. increased compant, and selecting for a modified trait (e.g. increased compant, and selecting for a modified trait (e.g. drought), microbial compant of a griculturally useful proteins or metabolic chemicals, possible tolerance, environmental stress response (e.g. drought), microbial companies of the companies of the companies of the companies of the prosent sequence is one of the 232 proteins which are constitution for trait in factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered trait as common to a wild-type or reference when the plant possesses are altered traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated or recombinant polynucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK65341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2001; 2001WO-US26189
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(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEND-)
(PILG/)
(CREE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KEDD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-292022/33.
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JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATCLIFF O. REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PINEDA O
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                                            transcription
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,, Yu G
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17-APR-2000;
22-AUG-2000;
     The present sequence is homologue G2421 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the insoluble sugar content of seeds, to modify the oil content of seeds and seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription factor; trait modification; structural characteristic; developmental cagricultural biotechnology.
vitamin and mineral content, to modify vitamin to modify the insoluble sugar content of content, to modify fatty acid and modify fatty acid and modify fatty acid.
                                                                                                                                                                                                                             Nucleic acids encoding plant transcription factor polypeptides, useful for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                         Claim 4; Page 116; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                               Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEND-)
(REUB/)
(CREE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                     (PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YUGG/)
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DB; AAD05768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILGRIM M.
RIECHMANN J
                                                                                                                                                                                                                                                                                                                                                                                                                 HEARD
                                                                                                                                                                                                                                                                                                                                                                                                                                   PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREELMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENDEL
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                                                                                                                                                                                                                                                                                                                                                          Creelman
Heard J;
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2000US-0197899.
2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characteristic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
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                                                                                                                                                                                                                                                                                                                                                                           Jiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agriculture; metabolic Gnemicol, virginitations and disease resistance; fruit yield; growth rate; leaf senescence; flower struit yield; growth rate; leaf senescence; flower struit yield; growth rate; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tolerance, seedling vigour, pest and pathogen resistance and germin rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
           (MEND-)
(PILG/)
(CREE/)
(DUBE/)
(HEAR/)
(JIAN/)
(XEDD/)
(ADAM/)
(RADM/)
(RAUB/)
(REUB/)
(REUB/)
(RIEC/)
(YUGG/)
                                                                                                                                                                                                                                                                     22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
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                                                                                                                                                                                                                                                                                                                                                                                                                  WO200215675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis transcription factor
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les 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to alter seed characteristics such as shelf-life, size, stress
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                                                                                                    KEDDIE J.
ADAM L.
                                                                                                                                        HEARD J.
JIANG C.
                                                                RATCLIFF O. REUBER J L.
                                                                                                                                                                          CREELMAN R.
DUBELL A J.
             PINEDA
                              RIECHMANN
YU G.
                                                                                                                                                                                                                PILGRIM M.
                                                                                                                                                                                                                                    MENDEL BIOTECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEPCCKTKIKRINIITPP-----NTPAQKVCENSITCNKDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSKGLRKGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DPWWINLLENCNDDIEEDEEV-VINYEKTLTSLLHEEISPPLNIGEGNSMOOGQISH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolic chemical; environmental stress;
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No. 1.7e-41;
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drought; ed yield;

EK---DDFVDNF

156 185 111

-KEGTLA-

79;

Gaps

126

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RESULT 13
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AC AAB68
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are a transgenic plant comprising the polynucleotides, a computer creadable medium having stored sequence information, and identifying a compound sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a composition of the polynucleotide or an antisense nucleic acid, inserting the polynucleotide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. drought), microbial composition of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial constitution flower sensescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 120
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09-JUL-2001
                                                                                                                          AAB68355 standard; Protein;
                                                                AAB68355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated or recombinant polynucleotide used to produce
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DB; ABK65362.
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Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       MVGDNIWLERL-----LDEGQEVDVLVTEAAATE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- DPWWINLLENCNDDIEEDEEV-VINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEPCCKTKIKRINIITPP----NTPAQKVCENSITCNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNKCGEISTK-IEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKGLRKGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.1%; Score 518.5; DB 23;
44.0%; Pred. No. 1.7e-41;
tive 29; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubell AJ, Heard J, on the state of the stat
                                                                                                                             211 AA
                                                                                                                                                                                                                                                                                          -FDVE-QLWNLFD 202
                                                                                                                                                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang C,
L, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EK---DDFVDNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      listed in the proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keddie J;
Pineda O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 known plant
I from one of
                                                                                                                                                                                                                                                                                                                                                                                                                           KEGTLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
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Best Local S
Matches 103
                                                                                                                                                                                                                                                                   enhancing a plant's tolerance or sensitivity to stress e.g. Salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, flavonoids, lignins, salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                                                                                                              The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes atmYB60, AtmYB764, AtmYB75 and AtmYB90. MYB polypeptides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                           derivatives.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 3B; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        Myloblastosis transcription factors for increasing stress resistance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1999;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2000; 2000WO-US30503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200132002-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-316365/33.
                        124 DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP----CLGLNINNVCDNS
160 VILDEEEHCKEIISEKQTPDASMDNVDPW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequence
                                                                                                    67
                                                                                                                                                                              103;
                                                                         64 GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKR
                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tolerance; myloblastosis transcription factor; anscription factor; AtMYB60; AtMYB764; AtMYB75;
                                                                                                                                                                             Similarity, 49.:
03; Conservative
                                                                                          GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK-------
                                                                                                                                           SSIGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                             SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                              a field
                                                                                                                                                                                                                                211
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2000US-0693855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                LNTTKIVPREK---INNKCGEIST--KIEIIKPQRRKYFSSTMKNVTNNN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of MYB transcription factor AtMYB75
                                                                                                                                                                                        34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tyr encoded by ATATAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gly encoded by TTTGGA"
                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by
                                                                                                                                                                            Score 510; DB 22;
Pred. No. 1.1e-40;
5; Mismatches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCGAT"
                                                                                                                                                                              43;
                                                                                                                                                                                                    Length 211;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat tolerance;
transgenic plan
                                                                                                                                                                              38;
                                                                                                                                                                             Gaps
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                        179
                                                                           123
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ARBSULT 14
ARAB2483
IID AABB8
XX AAB8
XX AAB8
XX AAB8
XX GhMY
XX GhMY
XX GhMY
XX GOSS
XX GOSS
XX WO20
XX WO20
XX WO20
XX WO21
PF 01-D
PF 01-D
PF 01-D
XX WPI;
DR N-PSI
XX WPI;
DR N-PSI
XX WPI;
DR N-PSI
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CCC The I
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Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor GhWB 7. The sequence was deduced from GhWB 7. DNA isolated from a Gossypium hirsutum cv. Acala SJ-2 10-day pre-anthesis fibre cDNA library. A claimed method of modulating transcription in a plant involves introducing into the plant a recombinant expression cassette comprising a promoter that is operably linked to a heterologous polynucleotide encoding a MYB protein, especially dhWRB 1 or GhWYB 6. The plant is especially a cotton plant, and the promoter directs expression of the polynucleotide in cotton fibres or roots. Valuable phenotypes can be conferred on the plant by this method, e.g. increased fibre quality, yield, length, strength or fineness, alteration of root architecture, and enhanced growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating transcription in plants for improving cotton fiber quality comprises introducing a recombinant expression cassette comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of cotton R2R3-MYB transcription factor GhMYB 7. The sequence was deduced from GhMYB 7 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 44; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-397938/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GhMYB 7; MYB; cotton; transcription factor; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999;
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                                 176
                                                                                                                                                123
                                                                                       124 AAPSKN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                          100;
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                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                         DIKRGNISPDEEELIIKLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLSKRVSDROKSP
                                                                                                                                                                                                                                          HIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVP 122
QTPDASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQ 235
                                                                                                                                                                                                                                                                                                                     SPCCSKEGLNRGAWTALEDKILKDYIKVHGEGRWRNLPKRAGLKRCGKSCRLRWLNYLRP 63
                                                                                                                                                                                                                                                                                                                                                                        STSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRP
                                                                                                                                          REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNN-----NVILDEEEHCKEIISEK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                                                                                                                    28.6%;
larity 37.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US32731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 422; DB 22;
Pred. No. 5.3e-32;
34; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a sequence encoding a MYB polypeptide
                                                                                       PEAARRGTAGNGNTNGNGSGSSSTHVVRTRATRCSKVFI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                          168
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B 성 B 성

70

> 68 69 123

Matches

Conservative

45;

Mismatches

91;

Indels

36;

Gaps

LGVRKGSWIDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGD

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RESULT 15
AAB33304
ID AAB33304
XX AAB33
XX AAB33
XX AAB33
XX AAB33
XX Plant
KW Pinus
XX Plant
KW Popla
KW Popla
KW Popla
KW Popla
XX Plant
KW Popla
KW PF 09-MJ
XX PINUS
PR 11-MJ
PR 11
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   Query Match
Best Local Similarity
                                                                                                                                                                                     The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins bZIP bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1999;
18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinus radiata transcription
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                                                                                                 Sequence
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                                                                                                                                                                 Сув2Нів2,
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FLETCHER CHALLENGE FORESTS LTD.
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                                                                                                                                                                 CCAAT box elements and MYB.
                                                                                                    391 AA;
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99US-0149485.
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Score 420; DB 21;
Pred. No. 1.2e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
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Search Job ti	Db	8	Db	Ş	DЬ	Ş	
Search completed: January 29, 2004, 20:11:24 Job time : 43 secs	237 HNKGSKQVPFPLSNTACENSSAQGVAGD 264	230 EGNSMQQGQISHENWGEFSLNLPPMQQGVQND 261	183 LPENQLLETSNSQCPSVATDFVPQAPSIPSTAYSFQQSTTSSVPGGVSDSVDVN 236	181 SMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIG 229	130 SESEDICSSPGNSEVSRKSQRENNAEIPRKVADGAVDIQDKEEDITEDQTSAQ 182	124EKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDA 180	

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 , Gapext 0.5
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1477
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 538		Length 248	BB	ID US-09-610-185C-2	Description
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. ω	370.5	•	278	N	-08-722-626B-	Sequenc
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80		16.3	156	w	-08-928-941D	Sequenc
9	240.5	16.3	156	4	-09-280-	Sequenc
10		16.0	156	ω	-08-928-941D-	Sequenc
11		16.0	156	4.	-09-280-590A-	Sequenc
12		10.7	802	w	-09-156-	Sequence
13	w		51	ш	-08-519-103-	Sequenc
14	138	9.3	51	Ь	-08-519-103-1	Sequence
15	138	9.3	51	ω	-09-018-635-1	Sequenc
16	138	9.3	51	ω	-09-018-635-1	Sequenc
17	138	9.3	51	4.	US-09-912-962-16	Sequence
18	138	9.3	51	4	-09-912-962-	Sequenc
19	135	9.1	51	_	-08-519-103-	Sequenc
20	135	9.1	51	ω		Sequenc
21	135	9.1	51	4	2	Sequenc
22	132		94	N	-030-	Sequenc
23	131	8.9	51	μ	-08-519-103-1	Sequenc
24	131		51	ω	-09-018-635-	Sequenc
25	. 131		51	4	-962-1	Sequence
26	127.5		372	ω	-08-928-941D	Sequence
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RESULT 2

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SISPPLNI	NTTKI DITPIPTPALKNNV VILDEBEHCKEIISE : : : : : : : : : : : : : : : : : :	H : : : : : :	Similarity 5; Conservat	185C-2 2, Application 6, 6573432 INPORMATION: NT: Borevitz, NT: Dixon, Rin NT: Lamb, Chr. FINTENTION: RIN FILLING DATE: PLICATION NUM ILLING DATE: 20 OF SEG ID NOS: OF SEG ID NOS: CF FASTSEQ FOR OF SEG ID NOS: CF SESTSEQ FOR OF SEG ID NOS: CF SEG ID NOS:		88 88 88 88 88 88 88 88 88 88 88 88 88
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EEISPPLNIGEGNSMOOGQISHENWGEFSLNLPPMOOGVONDDFSAEID- ; ; ; ; ; ; ; DILVPEATTTEKG	IVPREKINNKCGEISTKIEIIKPC		re 538; DB 4; d. No. 2.2e-48 Mismatches 4	HOCYANIN ,185C 44	ALIGNMENTS	-08-928-941D-1 -09-280-590A-1 -08-928-941D-29 -09-280-590A-29 -08-928-941D-35 -09-280-590A-45 -09-119-103-14 -09-156-316-5 -08-519-103-13 -09-12-962-13 -09-156-316-6 -09-156-316-6 -09-156-316-6 -09-153-277-2 -09-599-652-2
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DDFSAEID-LWNLLD 274 :: : DTLAFDVDQLWSLFD·241	RRKYESSTMKNUTINN		248; ls 86; Gaps	·		Sequence 1, Appli sequence 29, Appl sequence 29, Appl sequence 35, Appl sequence 45, Appl sequence 14, Appl sequence 14, Appl sequence 13, Appl sequence 13, Appl sequence 13, Appl sequence 13, Appl sequence 13, Appl sequence 14, Appli sequence 14, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli
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RESULT 3
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Best Local Similarity 48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Borevitz, Justin APPLICANT: Xia, Yiji
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: SALKINS.003C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
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NAME/KEY: VARIANT
LOCATION: (1)...(249)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                       APPLICANT: Yang, Yinong
APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: HOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                        SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              STREET: 1601
CTTY: Philadelphia
                                                                                  COMPUTER: IBM CONCERNING SYSTEM:
APPLICATION NUMBER: US/0 FILING DATE: 27-SEP-1996
                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 DEEEHCKEIISEKQTPDASMDNVDPWWINLLENCNDDIEEDEEVV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 KNIISPSTTPVOKIGVFKPRPRSFSVNNGCSHLNGLPXVDLIPSCLGLKKNNVCENSITC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                         E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                             USA
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                                                                                                        IBM Compatible
                                                                                                                              Diskette
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Pred. No. 3.1e-47;
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                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08997251 Patent No. 6271440
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                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
APPLICATT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
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ANTI-SENSE: NO
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LENGTH: 278 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
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                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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les 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                      COUNTRY: U
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                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          222 STDHVMVAANQELQVQLPFSSFKEENVDILATKMEDDMDFW 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 MGLKKGPWIPEEDQILISFIQTNGHGNWRALPKQAGLLRCGKSCRLRWTNYLRPDIKRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGD
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5370 Manhattan Boulevard
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US/08/997,251
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Pred. No. 9.8
                                  Version
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Best Local Similarity
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REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: AU PN3779/95
FILING DATE: 23-JUN-1995
                                                                                                                                                                                                           APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III
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APPLICATION NUMBER:
FILING DATE: 09-NOV-
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                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                   STREET: SURFICE Boulder
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                                                                COUNTRY:
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                                                                                                                                                 ADDRESSEE:
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                                                                                                                              5370 Manhattan Boulevard
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                                                                                                                                               Greenlee, Winner and Sullivan, P.C.
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                                                                                                                                                                                                                                                                                                                                 Patent No. 6410825
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Best Local Similarity
Matches 65; Conserv
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APPLICANT: Temple
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                                                                                                                                                                                             APPLICANT: Toscani, Antonio
APPLICANT: Hatton, Kimi
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
TITLE OF INVENTION: USES THEREOF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                          COUNTRY: U
ZIP: 19102
                                                                                  STATE:
                                                                                              ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. STREET: Suite 1800 Two Penn Center Plaza CITY: Philadelphia
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REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AEEERLIIQLHSKMGNKWARMAAHLPGRTDNEIKNYWNTRIKR---
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 amino acids
                                                          U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                             Temple University -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (303) 499-8080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU PN3779/95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110-97
                                                                                                                                                                                                                                                                                             Of The Commonwealth System of Higher Education
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SYSTEM:

YSTEM: PC-DOS/MS-DOS

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US-09-402-929-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, DANIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MONACO, DANIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND TITLE OF INVENTION: USES THEREOF
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                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                        ZIP: 19102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                   CLASSIFICATION:
                                                                                                                                                     FILING DATE:
                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 16.4%; Score 242.5; DB 4 socal Similarity 43.7%; Pred. No. 1.1e-16;
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Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toscani, Antonio
Hatton, Kimi
Reddy, E. P.
                                                                                                                                                                                                                                                                                                                         U.S.A.
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                                                                                              PCT/US98/06896
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   6056-214 PC
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                                 US-08-928-941D-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application Patent No. 6180763
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (215) 568-5549 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                              TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
                                                                  FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watch 16.4%; Score 242.5; DB 4 Local Similarity 43.7%; Pred. No. 1.1e-16
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/928,941D FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
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                                                  ORGANISM:
                                                                                                                                         TOPOLOGY:
                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
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                                                                                   internal
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Length 156;
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Query Match Best Local Similarity

16.3%; 43.7%;

Score 240.5; DB 3; Pred. No. 1.9e-17;

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                                                                                                                                       Matches. 45;
                                                                                                                                                                           Query Match
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                                                                                                                                                            Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hirai,
                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 EDRIIYOAHKRIGNRWAEIAKLIPGRIDNAIKNHWNSIMRRKV 156
                                                                                                    13 KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKL 115
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                               73 EVDLILRLHKLIGNRWSLIAGRIPGRTANDVKNYWNTNLLRKL 115
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/280,590A FILING DATE: 29-Mar-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                  KGPWTKEEDQRVIKLVQKYGPKRWSVI-AKHLKGRIGKQCRERWHNHLNPEVKKTSWTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Ave,
                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherr, Charles
Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bodner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                          16.3%; Score 240.5;
43.7%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/09280590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sarah M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYCLIN-D BINDING FACTOR, THEREOF
                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                         Mismatches
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                                                                                                                                                          No. 1.9e-17;
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Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                         DB 4; Length 156;
                                                                                                                                       37;
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                                                                                                                                         Indels
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                                                                                                                                                                       US-09-280-590A-46
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                                                                                                                    Sequence 46, Applicati Patent No. 6303772 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36,
                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hirai, APPLICANT: Sherr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
NUMBER OF SEQUENCES:
                                                                                                     APPLICANT: Hirai, Hiroshi
                                TITLE OF INVENTION:
                                                                                                                                                                                                                                            114 EDRIIYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV 156
                                                                                                                                                                                                                                                                                                                 55 KGPWTKEEDQRVIELVQKYGPKRWSVI-AKHLKGRIGKQCRERWHNHLNPEVKKTSWTEE 113
                                                                                                                                                                                                                                                                                                                                                  13 KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
                                                                                                                                                                                                                                                                           73 EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKL 115
                                                                                                                                    6, Application US/09280590A
6303772
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201-487-5800
                                                                 Sherr, Charles
Inoue, Kazushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 236.5; DB 3
42.7%; Pred. No. 4.9e-17;
rative 21; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYCLIN-D BINDING FACTOR, AND USES THEREOF
                                                                                     Charles
                                                  Sarah M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/928,941D
                CYCLIN-D BINDING FACTOR, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36:
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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ORGANISM: Gallus gallus sequence DESCRIPTION: SEQ ID NO: 46: US-09-280-590A-46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-156-316-1
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US-09-156-316-1
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Best Local Similarity
                                                              SEQ ID NO 1
LENGTH: 802
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09156316
Patent No. 6183961
                                                                                                                                                   APPLICANT: Bernstein, Harold S.
APPLICANT: Coughlin, Shaun R.
TITLE OF INVENTION: Methods and Compositions for Regulating Cell Cycle
TITLE OF INVENTION: Progression
FILE REFERENCE: UCSF-020/01US
CURRENT APPLICATION NUMBER: US/09/156,316
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 60/060,688
EARLIER FILING DATE: 1997-09-22
                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-343 1684
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,590A
FILLING DATE: 29-Mar-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 EDRIIYQAHKRIGNRWAEIAKLIPGRTDNAIKNHWNSTMRRKV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGPWTKEEDORVIELVOKYGPKRWSVI-AKHLKGRIGKOCRERWHNHLNPEVKKTSWTEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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42.7%;
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RESULT 14 US-08-519-103-17

Sequence 17, Application US/08519103 Patent No. 5733730

GENERAL INFORMATION:

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                                                               Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: deLang
                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E.
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/519,103 FILING DATE: 25-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TTDDPRKL---KPGEIDPNPE-TKPAR------PDPIDMDEDE--LEMLSE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TKIVPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 IKKTEWSREEEEKLLHLAKLMPTQWRTIA-PIIGRTAAQCLEHYEF-LLDKAAQRDNEEE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 IKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKL-----NT 117
                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRI---ASLLHRKSAKQCKARWYEWLDPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 MSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGL--NRCRKSCRLRWLNYLRPH
1 VKKSSWTEEEDRIIYEAHKRIGNRWAEIAKLIPGRTDNSIKNHWNSTMRRK 51
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                                                                                                                                                                                                 : 51 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hackensack
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                                                                                                                                                                                                                                                                                                                                                    36,113
                                                                                                                                                                                                                                                      16:
                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                           600-1-142
                                                                  Score 138; DB 1; 1
Pred. No. 2.1e-07;
1; Mismatches 16;
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                                                                                                Length 51;
                                                                  Indels
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US-08-519-103-17
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018.635
FILING DATE:
CLASSTETT
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09018635
Patent No. 6297356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E.
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: line
YOLECUT.P
                                                                                                                                                                                                                                                                APPLICANT: Broccoli, Dominique
APPLICANT: Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESCEPT TO THE ADDRESS:
ADDRESCEPT TO THE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
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                                                                                                                                                                                             STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey
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CITY: Hackensack
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                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 138; DB 1;
49.0%; Pred. No. 2.1e-07;
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TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
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Search completed: January 29, 2004, 20:13:54 Job time : 22 secs
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                                                                                                                                                                                                                                 US-09-018-635-16
                                                                                                                                                          Matches
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: David A. Jackson
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                      Local Similarity
nes 24; Conserv
                                                                                                                64 IKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK 114
                                                                               1 VKKSSWTEEEDRIIYEAHKRIGNRWAEIAKLIPGRTDNSIKNHWNSTMRRK 51
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                                                                                                                                                                        9.3%;
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Pred. No. 2.1e-07;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model "

Run on: January 29, 2004, 20:12:52; Search time 33 Seconds (without alignments) 1725.570 Million cell updates/sec

US-10-033-190-2 1477

Title: Perfect score: 1 MNSTSMSSLGVRKGSWTDEE.....QQGVQNDDFSAEIDLWNLLD 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US09A PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10 PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
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6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:* 6/ptodata/1/pubpaa/US08 NEW PUB.pep:* 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	13	12	11	10	9	œ	7	6	₅	4	ω	8	_	Result No.
394	396.5	397	401	401	408	408	423.5	518.5	524	532.5	532.5	542.5	1477	Score
26.7	26.8	26.9	27.1	27.1	27.6	27.6	28.7	35.1	35.5	36.1	36.1	36.7	100.0	Query Match Length
363	302	342	203	203	269	269	249	209	212	249	249	246	274	Length
12	. 0	11	12	11	15	11	15	11	11	15	11	11	14	DB
US-10-093-837-2	US-09-443-704-12	US-09-934-455-252	US-10-407-920-29	US-09-934-455-390	US-10-278-173-72	US-09-533-029-94	US-10-286-264-148	US-09-934-455-480	US-09-934-455-438	US-10-295-403-44	US-09-934-455-14	US-09-934-455-482	US-10-033-190-2	ID
Sequence 2, Appli	Sequence 12, Appl	Sequence 252, App	Sequence 29, Appl	Sequence 390, App	Sequence 72, Appl	Sequence 94, Appl	Sequence 148, App	48	43	Sequence 44, Appl	14,	Sequence 482, App	Sequence 2, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
368	368	368	368.5	370	370	370	371	373	373	373.5	373.5	374	374	374	374	374	377	377	377	377	377.5	379.5	379.5	385	385	387.5	387.5	393	393
24.9				25.1			25.1		25.3					25.3								25.7		26.1	26.1	26.2	26.2	26.6	26.6
305	120	120	333	245	149	149	332	282	281	335	295	371	371	371	273	273	349	349	268	268	274	258	258	246	246	253	253	120	120
9	14	9	15	15	14	9	15	12	15	15	15	16	11	11	14	9	16	15	14	9	16	14	ø	14	9	14	9	14	9
US-09-443-704-8	US-10-008-118A-50	US-09-443-704-50	US-10-278-173-146	US-10-295-403-60	US-10-008-118A-30	US-09-443-704-30	US-10-021-811-54	US-10-225-068-10	US-10-295-403-46	US-10-295-403-58 ·	US-10-278-173-152	US-10-278-536-40	US-09-934-455-66	US-09-533-029-86	US-10-008-118A-20	US-09-443-704-20	US-10-278-536-114	US-10-278-173-138	US-10-008-118A-34	US-09-443-704-34	US-10-278-536-36	US-10-008-118A-4	US-09-443-704-4	US-10-008-118A-32	US-09-443-704-32	US-10-008-118A-28	US-09-443-704-28	US-10-008-118A-6	US-09-443-704-6
Ü	e 50	50, ,	146	60,		30,	54	10,	46	Sequence 58, Appl	152	40,	66,	86,	e 20	20, 1		138,	e 34	w	Sequence 36, Appl	e 4	-	Sequence 32, Appl	32	e 28,	•	Sequence 6, Appli	Sequence 6, Appli

ALIGNMENTS

RESULT 1 US-10-033-190-2

1 VQ	Оу 1 рь 1	B &	9 8 8	Query Match Best Local Matches 27	Sequence 2, A Publication N GENERAL INFOR APPLICANT: E TITLE OF INV TITLE OF INV FILE REFEREN CURRENT APPL CURRENT APPL CURRENT FILI PRIOR FILING PRIOR FILING NUMBER OF SE SOFTWARE: PA SEQ ID NO 2 LENGTH: 274 TYPE: PRT COGGANISM: L TYPE: PRT COGGANISM: L TYPE: PRT COGGANISM: L TYPE: PRT COGGANISM: L C COGGANISM: L COGGANISM: L C COGGANISM: L C C C C C C C C C C C C C C C C C C C
181 SMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS 240	121 VPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDA 180 	61 RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKI 120 	1 MNSTSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYL 60 	Query Match 100.0%; Score 1477; DB 14; Length 274; Best Local Similarity 100.0%; Pred. No. 2.3e-135; Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 2, Application US/10033190 Publication No. US20020133848A1 GENERAL INFORMATION: APPLICANT: Exelixis Plant Sciences, Inc. TITLE OF INVENTION: TOENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT TITLE OF INVENTION: TOMOROUS FILE REFERENCE: EP01-002C CURRENT APPLICATION NUMBER: US/10/033,190 CURRENT APPLICATION NUMBER: US 60/244,685 PRIOR APPLICATION NUMBER: US 60/244,685 PRIOR FILING DATE: 2000-10-30 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PatentIn version 3.1 SEQ ID NO 2 LENGTH: 274 TYPE: PRT ORGANISM: Lycopersicon esculentum -10-033-190-2

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US-09-934-455-14
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; SEQ ID NO 482
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-482
                                                                      Sequence 14, Application US/099 Publication No. US20030121070A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 482, A Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                     APPLICANT: Adam, APPLICANT: Cree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR TILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
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CURRENT FILING DATE: 2001-08-22
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TITLE OF INVENTION: Genes for Modifying Plant
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                                                                                                                                                                                               183 CNKDEQKDKLININLLDGDNMWWESLLE 210
                                                                                                                                                                                                                                                                    123 NKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSIT 182
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                                                                                                                                                                                                                                                                                                                                        GKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMI- 122
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                                                                                                                                                                                                                                                                                                                                                                                                             SPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKPSIKR
Creelman, Robert
Dubell, Arnold
Heard, Jacqueline
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Heard, Jacqueline
Jiang, Cai-Zhong
                                                                                                     Application US/09934455
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Yu, Guo-Liang
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b. US20030121070A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
                APPLICANT: Fromm, Mike
TITLE OF INVENTION: PLANT GENE SEQUENCES I
FILE REFERENCE: MBI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT FILING DATE: 2002-11-15
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         PRIOR APPLICATION NUMBER: US/09/394,519
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                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                        Keddie, James
Zhang, James
Benito, Maria-Ines
Yu, Guo-Liang
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Reuber, Lynne
Jiang, Cai-Zhong
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Adam, Luc
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; ORGANISM: Arabidopsis thaliana US-09-934-455-14
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PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
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TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
                                           241 HENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
                                                                                                                       184 NVDPWWINLLEN---CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS 240
                                                                                                                                                                                         124 KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
                                                                                                                                                                                                                                         127 NNKCGEIST---KIEIIKPORRKYFSSTMKOVTNNNVILDEEEHCKEIISEKOTPDASMD 183
                                                                                                                                                                                                                                                                                                                                                                                                                    7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
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Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
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GEN-QEADAIVPEATTAEHGATLAFDVEQLWSLFD
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Pred. No. 1.6e-43;
4; Mismatches 76
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242
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US-10-295-403-44
              PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
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LENGTH: 249
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/101,349
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
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PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/934,455
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SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
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Jiang, Cai-Zhong
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o. US20030121070A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 480
LENGTH: 209
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LENGTH: 212
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-22.
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
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APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
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                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 -----LNTTKIVPREK---INNKCGEIST--KIEIIKPQRRKYFSSTMKNVTNNN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 VILDEEEHCKEIISEKQTPDASMDNVDPWWI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP----CLGLNINNVCDNS
                                                                                                                                                   120;
64 GKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                          4
                                                                                                  7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGINRCRKSCRLRWLNYLRPHIKR
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                      GDFEQDEVDLILKLHKKLLGNRWSLIAGRLFGRTANDVKNYWNTNLLRKLNTTKIVFREKI 126
                                                                        SSKGLRKGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
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Pilgrim, Marsha
Ratcliffe, Oliver
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Jiang, Cai-Zhong
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                                                                                                                                                     Conservative
                                                                                                                                                 35.1%; Score 518.5; DB 1
44.0%; Pred. No. 2.9e-42;
vative 29; Mismatches 45
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                                                                                                                                                                                       DB 11; Length 209;
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; SEQ ID NO 148
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G211
US-10-286-264-148
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APPLICANT: Riechmann, Jos
APPLICANT: Riechmann, Jos
APPLICANT: Zhang, James
APPLICANT: Zhang, Cai-Zho
APPLICANT: Pineda, Omaira
APPLICANT: Heard, Jacquel
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 199-03-23,
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Reuber, Lynne
APPLICANT: Pilgrim, Marsha
APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED
FILE REFERENCE: MBI-008
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                                                                           172
221
                                     229
                                                                                                                                                    136 --
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                                                                                                                181 SMDNVDPWWINLLE------NCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNI 228
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                                                                                                                                                                                                                                                                                                      19 TKMGMKRGPWTVEEDEILVSFIKKEGEGRWRSLPKRAGLLRCGKSCRLRWMNYLRPSVKR 78
                                                                                                                                                                                                                                                                                                                                   7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR 66
                                                                                                                                                                                       NNKCGEISTKIEIIKPORRKYFSSTMKNVTNNNVILDEEE-----HCKEIISEKOTPDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVGDNIWLERL-----LDEGQEVDVLVTEAAATE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNKCGEISTK-IEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENWGEFSLNLPPMQQGVQNDDFSAEIDLWNLLD 274
                                                                           TVNGGDGDSKNSINVFGGEHGYEDFGFCYDD-----KFSSFLNSLIN-DVGDPFG-
                                                                                                                                                                                                                               GGITSDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNYWNTHLRKKLLRQGIDPQ--- 135
                                                                                                                                                                                                                                                  GDFEQDEVDLILKLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKIVÞREKI 126
                                   GEGNSMQQGQISHENWGEFSLNLPPMQQGVQNDD
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Ratcliffe, Oliver
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Heard, Jacqueline
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b. US20030093837A1
----NIIPISOPLOMDD 233
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                                     262
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APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Hander, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MB1-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
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US-10-278-173-72
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                                                                                                                                                                            Sequence 72, Application US/10278173 Publication No. US20030061637A1 GENERAL INFORMATION:
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Publication No. US20030046723A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity 39.7%;
Matches 96; Conservative 3
                    APPLICANT:
                                                           APPLICANT:
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APPLICANT: Ratcliffe, Oliver
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APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
                                                                                                  APPLICANT:
                                                                                                                                         APPLICANT: Jiang, Cai-Zhong APPLICANT: Broun, Pierre
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 MNKGAWTKEEDERLVSYIKSHGEGCWRSLPRAAGLLRCGKSCRLRWINYLRPDLKRGNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 VRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEE---RVVVEEKIGP
                                                         Riechmann, Jose-Luis
Pineda, Omaira
Zhang, James
Yu, Guo-Liang
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                  Pilgrim, Marsha
Keddie, James
Heard, Jacqueline
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; Pred. No. 2.3e-31;
37; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
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APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
FILE REFERENCE: MBI-009
CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR PILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 72
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US-10-278-173-72
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                         APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                 PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
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APPLICANT: Creelman, Robert
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TYPE: PRT
APPLICATION NUMBER: MBI-0023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 DASMD-NVDPWWINLLE--NC-----NDDIEEDEEVVINYEKTLTSLLHEEIS-PPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 AKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEE----RVVVEEKIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 HDEDELIIKLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIKRKLLSKGIDPATHRGINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVP--REKINN 128
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Jiang, Cai-Zhong
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Ratcliffe, Oliver
Adam, Luc
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Pilgrim, Marsha
Ratcliffe, Oliver
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Riechmann, Jose Luis
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                  Dubell, Arnold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09934455
b. US20030121070A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 269;
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RESULT 12
US-09-934-455-252
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; LENGTH: 203
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-407-920-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shi, Lifang
TITLE OF INVENTION: MYB Transcription Factors and
FILE REFERENCE: 38-21(52703)A
CURRENT APPLICATION NUMBER: US/10/407,920
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US/60/370,759
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
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Sequence 252, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.:
SEQ ID NO 390
LENGTH: 203
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Best Local Similarity
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                                                                                                                                                                                           132 EISTKIEIIKPQRRKYFSSTMKNVTNNNVILDE--EEH 167
                                                                                                                                                                                                                                                           72 DEVDLILKLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKIVÞREKINNKCG
                                                                                                                                                                                                                                                                                                                        17 KKGLWTVEEDKILMDYVKAHGKGHWNRIAKKTGLKRCGKSCRLRWMNYLSPNVKRGNFTE
                                                                                                                                                                                                                                                                                                                                              12 RKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 KKGLWTVEEDKILMDYVKAHGKGHWNRIAKKTGLKRCGKSCRLRWMNYLSPNVKRGNFTE 76
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                                                                                                                                                  DIVYOINLPNPTETSEETKISNIVDNNNILGDEIQEDH 170
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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48.7%; Pred. No. 7.6e-31;
Vative 26; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.1%; Score 401; DB 11; 48.7%; Pred. No. 7.6e-31;
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APPLICANT: Adam, Luc APPLICANT: Creelman, Robert APPLICANT: Dubell, Arnold APPLICANT: Heard, Jacqueline APPLICANT: Jiang, Cai-Zhong

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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Ciu, Zhan-Bin
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
CURRENT APPLICATION NUMBER: US/09/443,704
CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: 60/109,294
EARLIER FILING DATE: NO. US20020066120Alember 20, 1998
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US-09-443-704-12
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 252
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                                                                                                                                                                                                                                                                               Sequence 12, Application US/09443704
Patent No. US20020066120A1
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Best Local
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PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
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TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
                   NUMBER OF
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GDNSSCCVNLFEEEQGSETKIGHVGITEVDHDMTVEREREGSFLSSNSNENNDKDWWVGL 300
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Similarity 31.9%;
SEQ ID NOS: 50
Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                              CNSSEVGFGVDEELLDWEFQGNVTCQSDDLWDLSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                  LNLPPMQQGVQND----DFSAEI-----DLWNLLD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKELESDFSEGGQNGNFEGESLGPYEWLDGELERLLSSCVWECTSEEAVIGVNDEKVCES
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Ratcliffe, Oliver
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Pred. No. 3.8e-30;
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US-10-008-118A-12
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LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/10008118A
Publication No. US20020187539A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 USDIV
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
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TH: 302
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   251 LPPMQQG 257
                                                                                                                                                                                                             73 EVDLILRLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKIVPR--EKINNKC 130
                                                                                                                                                                                                                                                                   14 KGAWTKEEDERLINYIKLHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE
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                                                                                                                                                                                                                                                                                         KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD
                                                                          NLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISHENWGEFSLN
                                                                                                                 TPATTATATAVPS----ANSSKKINNNN
                                                                                                                                                    GEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNVDPWWI 190
                                       NDINNNNNGFQLVSNSAYANTKIGTNLVAAEDS---NSSSGVTTEESVPHHQLNLDLSIG
                                                                                                                                                                                           EDELIINLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIKRKLYSRGIDPQTHRPLNASA 133
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                                                                                                                                                                                                                                                                                                                                              36; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Score 396.5; DB 14; Pred. No. 3.6e-30;
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Indels 37;

Gaps

73

-NNID----

161

Length 302

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191 NILENCNDDIEEDEEVVINYEKTLTSLIHEEISPPLNIGEGNSMOOGQISHENWGEFSLN
                                                                                                   134 TPATTATATAVPS-----ANSSKKINNNN---------NNID----
                                                                                                                                                    131 GEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNVDPWWI 190
                                                                                                                                                                                                                                  73 EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPR--EKINNKC 130
                                                                                                                                                                                                                                                                                                             14 KGAWTKEEDERLINYIKLHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE
                                                                                                                                                                                                                                                                                                                                                           KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD
NDINNNNNGFQLVSNSAYANTKIGTNLVAAEDS---NSSSGVTTEESVPHHQLNLDLSIG
                                                                                                                                                                                                         EDELIINLHSLIGNKWSLIAARLPGRTDNEIKNYWNTHIKRKLYSRGIDPQTHRPLNASA 133
                                                                                                                                                                                                                                                                                                                                                                                                                 26.8%; Score 396.5; DB 9
37.2%; Pred. No. 3.6e-30;
ative 36; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                   82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                   37;
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  218
                                                     250
                                                                                                         161
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Sequence 2, Application US/10093837

Publication No. US20030150011A1

GENERAL INFORMATION:
APPLICANT: Grotewold, Erich
APPLICANT: Dias, Anusha P.
APPLICANT: Dias, Anusha P.
APPLICANT: Braun, Edward L.
TITLE OF INVENTION: TRANSGENIC PLANTS WITH ALTERED LEVELS OF PHENOLIC COMPOUNDS
FILE REFERENCE: 22727/04082

CURRENT APPLICATION NUMBER: US/10/093,837

CURRENT APPLICATION NUMBER: 60/274,629
PRIOR APPLICATION NUMBER: 60/274,629
PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENCTH: 363
LENCTH: 363
CURRENT HARDEN COMPONISM: maize ZmMyb-IF-35 protein
US-10-093-837-2
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Search completed: January 29, 2004, 20:18:24
Job time : 34 secs
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US-10-093-837-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.7%; Score 394; DB 12; Length 363; Best Local Similarity 33.0%; Pred. No. 8.1e-30; Matches 99; Conservative 56; Mismatches 97; Indels 49
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219 LPSQPQG 225
                                                                                               239 LLAPE-SPKLEVGPDGSCMDSYSGPPSGESGCGSSGPSGDVAQDLDLDDDKAIMD-WDLM 296
                                                                                                                                           217 LIHEEISPPLNIG-EGNSMQ--QGQISHENWGEFSLNLPPMQQGVQNDDFSAEIDLWNLL 273
                                                                                                                                                                                            185 SVSTPRPQSDDCGTAQSEEEQAQASASGLTS-----DGHGPEEEEEEEDPLALSEEMVSA 238
                                                                                                                                                                                                                                     168 -----CKEIISEKQTPDASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTS 216
                                                                                                                                                                                                                                                                                      130 SKLPGGGK--RRGGRASRGAVVAAAKEKK---AKEKDDRGNSKVAEAEQQLRDTEDDDGG 184
                                                                                                                                                                                                                                                                                                                                  118 TKIVPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEH------
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Post-processing: Minimum Match 0%
Maximum Match 100%

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seq length: 2000000000 US-10-033-190-2 1477 1 MNSTSMSSLGVRKG BLOSUM62 283308 seqs, 96168682 residues Gapop 10.0 , Gapext 0.5 January 29, 2004, 20:09:31; Search time 20 Seconds MNSTSMSSLGVRKGSWTDEE... Copyright GenCore version 5.1.6 (c) 1993 - 2004 CompuçQQGVQNDDFSAEIDLWNLLD (without alignments)
1317.511 Million cell updates/sec Compugen Ltd 283308 274

Database PIR 76:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 2 B96608

probable transcription factor F25P12.92 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

ALIGNMENTS

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; 1 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96689 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000 hypothetical protein T27F4.12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A96689 밁 Ş 밁 Ś 밁 S ঠ A; Map position: 1 A; Gene: T27F4.12 A;Status: preliminary A;Molecule type: DNA A;Cross-references: GB:AE005173; NID:g10092494; PIDN:AAG12894.1; GSPDB:GN00141 A;Residues: 1-246 <STO> A96689 RESULT 1 Matches 109; Query Match y Match 36.7%; Local Similarity 52.4%; 168 123 123 64 67 NKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSIT 182 GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLN----TTKIVP 122 SSIGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR C-KEIISEKQTPDASMDNVDPWWINLLE 194 REKINNKCGEISTKIEIIKPORRKYFSSTMKNVT----SPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKPSIKR CNKDEQKDKLININLLDGDNMWWESLLE 210 GKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMI- 122 Conservative 26; Mismatches Score 542.5; DB 2 Pred. No. 1.3e-32; DB 2; P.; Southwick, A.M.; Sun, H.; Tallon, Indels Length 246; -NNNVILDEEEH 167 21; Gaps 63 66 Marziali,

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C;Accession: B96608
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                             A; Gene: MYB90
C; Superfamily:
C; Keywords: tr
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
T51687
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C;Superfamily: Arabidopsis 28K leaf-specific
                                                                                                                                                                                                                                                           Plant J. 16, 263-276, 1998
A; Title: Towards functional
                                                                                                                                                                                                                                                                                                                          myb-related transcription factor MYB90 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-200 C;Accession: T51687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-248 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A86141;
A;Accession: B96608
                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-249 <KRA>
A;Cross-references: EMB
                                                                                                                                                                                                                           A; Reference number: Z14349;
A; Accession: T51687
                                                                                                                                                                                                                                                                                            R;Kranz, H.D.; Denekamp, M.; Greco, ; Paz-Ares, J.; Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                         A; Status: preliminary; translated
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Best Local :
                             Query Match
Best Local :
                                                                                            Superfamily: Arabidopsis
             Matches
                                                                             Keywords: transcription
                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 NNKCGEI-----STKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHE-----PCCKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEES-QEVDILVPEATTTEKGDTLAFDVDQLWSLFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMKKRDITPIPTTPALKUNVYKPRPRSF-----TVNN-----DCNHLNAPPKV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
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               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE005173;
                                                                                                                                              EMBL:AF062915; PIDN:AAC83637
ce: cultivar Columbia
                         36.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.2%; Score 535; DB 2; 44.2%; Pred. No. 4.6e-32;
                                                                              factor
                                                                                        28K leaf-specific myb-related
                                                                                                                                                                                                                                             characterisation of the members MUID:9839469; PMID:9839469
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                             Score 532.5; DB 2; Pred. No. 7.1e-32;
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               Mismatches
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                                            Length 249;
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               43;
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B96689
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change C;Accession: B96689
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kau
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C;Keywords:
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, A.; Ecker, J.R.; Palm,
; Chung, M.K.; Conn, L.;
; Hughes, B.; Huizar, L.
816-820, 2000
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R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51680
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myb-related transcription factor MYB75 [imported] - Arabidopsis C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change C;Accession: T51680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-212 <KRA>
A;Cross-references: EMBL;AF062908; PIDN:AAC83630.
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                           transcription factor
                                                                                                                                                                                                                                                                          SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
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                                   VILDEEEHCKEIISEKQTPDASMDNVDPWWI
                                                                                DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP---
                                                                                                                        -----LNTTKIVPREK---INNKCGEIST--KIEIIKPQRRKYFSSTMKNVTNNN 159
                                                                                                                                                                                            GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK-----
                                                                                                                                                                                                                                                        SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                             35.5%;
48.3%;
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Pred. No. 2.4e-31;
-NLIDGDNMWL
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                                     190
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C.J.; Federspiel, N.A.; Kaul, S.; W Conway, A.B.; Conway, A.R.; Creasy,

#text_change

02-Aug-2002 S.; White, (reasy, T.H.;

o :.

Alonso, war, K.;

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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                     A;Introns: 99/3
C;Superfamily: Arabidopsis myb-related protein 5; myb DNA-binding repeat homology C;Keywords: DNA binding; duplication; nucleus; transcription regulation E;20-72/Domain: myb DNA-binding repeat homology <MYB1>
E;73-123/Domain: myb DNA-binding repeat homology <MYB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: T27F4.13
A;Map position: 1
C;Superfamily: Arabidopsis myb-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Li, S.F.; Santini, J.M.; Nicolaou, O.; Parish, R.W. FEBS Lett. 379, 117-121, 1996
A;Title: A novel myb-related gene from Arabidopsis th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005173; NID:g10092496; PIDN:AAG12896.1; GSPDB:GN00141C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-139 <ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Nov-1996 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myb-related protein 5 - Arabidopsis thaliana N;Alternate names: protein Atmyb5
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A; Residues: 1-249 <L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S68688; MUID: 96225952;
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  136
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                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                         NNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEE-----HCKEIISEKQTPDA 180
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                                                                                                                                                                               TKMGMKRGPWTVEEDEILVSFIKKEGEGRWRSLPKRAGLLRCGKSCRLRWMNYLRPSVKR
                                                                                     GGITSDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNYWNTHLRKKLLRQGIDPQ---
                                                                                                                              GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
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                                                                                                                                                                                                                                                                                       28.7%;
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MUID:96225952; PMID:8635574
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                                                                                                                                                                                                                                                                                       Score 423.5; DB 1
Pred. No. 6.8e-24;
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Pred. No. 4.6e-30;
                                                                                                                                                                                                                                                                  Mismatches
  THKPLDANNIHKPEEEVSGGQKYPLEPISSSHTDDT 171
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                                         T03974
c;Species: 2
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A;Map position: 2
A;Introns: 88/2
A;Introns: 88/2
C;Superfamily: barley myb-related protein 1; myb DNA-binding C;Keywords: DNA binding; duplication; nucleus; transcription C;Keywords: DNA binding; duplication; nucleus; transcription F;9-61/Domain: myb DNA-binding repeat homology <MYBI>
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A;Residues: 1-269 <QUA>
A;Cross-references: EMBL:X90385; NID:g928968; PIDN:CAA62033.1; PID:g928969
A;Cross-references: EMBL:X90385; NID:g928968; PIDN:CAA62033.1; PID:g928969
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.; l
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
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R;Quaedvlieg, N.E.M.; Dockx, J.; Keultjes, G.G.M.; submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable MYB family transcription factor At2g16720 [imported] - Arabidopsis thaliana N;Alternate names: myb-related protein Y49 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Datc: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 02-Mar-2001 C;Datc: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84543
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A; Residues: 1-269 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNKGAWTKEEDERLVSYIKSHGEGCWRSLPRAAGLLRCGKSCRLRWINYLRPDLKRGNFT 71
                                                                                                                        DINLELRISPPWONQREISTCTASRFYMENDMECSSETVKCQTENSSSISYSSIDISSSN
                                                                                                                                                                                   DASMD-NVDPWWINLLE--NC-----NDDIEEDEEVVINYEKTLTSLLHEEIS-PPLN
                                                                                                                                                                                                                                                AKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEE---RVVVEEKIGP
                                                                                                                                                                                                                                                                                                              -KCGEI-STKIEIIK------PQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTP 178
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Plant Cell 5, 1807-1816, 1993
A;Title: Role of the regulatory gene pl in
A;Reference number: Z15034; MUID:94138244;
A;Accession: T03974
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A;Title: Towards functional characterisation of the members A;Reference number: Z14349; MUID:9839469; PMID:9839469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable transcription factor MYB3 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51631
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F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
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A;Accession: T51631
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A;Experimental source: strain Tx303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
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                                                                                                   CGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCK-EIISEKQTPDASMDNVDPW
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                                                                                                                                      EEEDELIIKLHSLLGNKWSLIAGRLPGRIDNEIKNYWNTHIKRKLLSRGIDPNSHRLINE
 - IGMVNNCESSGTTSEKDYGNEEDWVLNLELSVGPSYRYESTRKVSVVDSAE---
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                               -DIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISH
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Pred. No. 1
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Pred. No. 2.1e-22;
                                                                   -SSLQNDVVETIHLDFSGPVKPEPVREE-
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A;Introns: 45/1; 88/2
A;Introns: 45/1; 88/2
C;Superfamily: barley myb-related protein 1; myb DNA-binding C;Keywords: DNA binding; duplication; nucleus; transcription E;9-61/Domain: myb DNA-binding repeat homology <MYB1> F;62-112/Domain: myb DNA-binding repeat homology <MYB2>
                                                                                                                                                                     myb-related protein - upland cotton
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #te:
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                   A; Molecule type: mRNA
A; Residues: 1-226 < LOG>
                                                 A; Status: preliminary; translated
                                                                   A; Reference number: A; Accession: T09773
                                                                                                        A; Description: Structure
                                                                                                                      R;Loguercio, L.L.; Zhang, J.; Wilkins, T.A. submitted to the EMBL Data Library, November 1997
                                                                                                                                      R;Loguercio,
                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                             T09773
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A; Residues: 1-257 < VYS>
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A; Accession: T00780
     A;Cross-references: EMBL:AF034134;
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Similarity 37.3%;
                                                                                                                                                          T09773
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                                                                                                                                        Zhang, J.; Wilkins,
                                                                                       Z16842
                                                                                                   and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                   DIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 403; DB 2;
Pred. No. 2.2e-22;
11; Mismatches 68
                                                     from
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSLONDVVETIHLDFSGPVKPEPVREE
     NID:g2921339; PID:g2921340
                                                                                                                                          T.A.
                                                                                                                                                                        16-Jul-1999 #text_change
                                                     GB/EMBL/DDB
                                                                                                        XTS
                                                                                                          classes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 257;
                                                                                                          얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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repeat homology regulation

Kwan, A.; Liu, S.; L: er, J.R.; Federspiel,

S.; Li, z

complete

44;

Gaps

70

111111111

163

TS

216

myb-domain

genes in allotetrap

19-May-2000

source:

cultivar

Acala

SJ-2; ovule

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A; Experimental (C; Genetics: A; Note: Cmy-O C; Superfamily: C; Keywords: DNA F; 8-60/Domain: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myb transcription factor werewolf WER/MYB66 - Arabidopsis thaliana N;Alternate names: protein T9L3_50 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51420 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tal submitted to the Protein Sequence Database, August 2000
myb-related protein - upland cotton
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
                                                                                 RESULT
T09744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 49/1; 92/2
A;Note: T9L3_50
C;Superfamily: trichon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z25394
A;Accession: T51420
A;Status: preliminary
                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-203 <SAT>
A;Cross-references: EMBL:AL391149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Note: T9L3_50;Superfamily: trichome differentiation protein GL1; myb DNA-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: unassigned Keywords: DNA binding; t
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                 RKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D---LDLTIAFPSSPIKNI---IEESQQKTASIVTNDEEEQYTVPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNQYPHHVGPLNPTTTNSMDVACKLRVCSTDNDDGISDAASYL----EDATPPTGISNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKINNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVRKGSWIDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDF
                                                                                                                                                          DIVYQINLPNPTETSEETKISNIVDNNNILGDEIQEDH
                                                                                                                                                                                              EISTKIEIIKPORRKYFSSTMKNVTNNVILDE--EEH 167
                                                                                                                                                                                                                                                                          DEVOLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKINNKCG
                                                                                                                                                                                                                                                                                                               KKĞLWTVEEDKILMDYVKAHGKĞHWNRIAKKTĞLKRCĞKSCRLRWMNYLSPNVKRĞNFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPWWINL-----LENCNDDIEEDEE----VVINYEK---TLTSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGEISTKIEIIKPQRRKYFSSTMK----NVTNNNVILDEEEHCKEIISEKQTPDASMDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIKRKLMKMGIDPN---NHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTNKGAWSKQEDQKLIDYIRIHGEGCWRSLPKAAGLHRCGKSCRLRWINYLRPDIKRGNF
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myb DNA-binding repeat proteins; myb DNA-binding repeat homole
transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                           27.1%; Score 401; DB 2; Length 203 48.7%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 402.5; DB 2; 41.7%; Pred. No. 2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat
                                                                                                                                                                                                                                                                                                                                                                                         26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.104; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1e-22;
ches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <MYB>
                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kotani, H.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                      IKDQKTKQSNG
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                                                                                                                                                                                                                                                                        131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129
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                                                                                                                                                                                                                                      132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
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70

EQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK

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A;Description: transcriptional activator for anthocyanin biosynthesis C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-b: F;9-61/Domain: myb DNA-binding repeat homology NYB>
                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T03972
R;Cone, K.C.; Cocciolone, S.M.; Moehlenkamp, C.A.; Weber, T Plant Cell 5, 1807-1816, 1993
A;Title: Role of the regulatory gene pl in the photocontrol A;Reference number: Z15034; MUID:94138244; PMID:8305873
A;Accession: T03972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
T03972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF034131; NID:g2921333; | A;Experimental source: cultivar Acala SJ-2; ovule C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T09744
R;Loguercio, L.L.; Zhang, J.; Wilkins, T.A.
submitted to the EMBL Data Library, November 1997
A;Description: Structure and expression of six cli
밁
                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:L19495; NID:g309569; PIDN:AAA19821.1; PID:g309570
A;Experimental source: strain McClintock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: DNA binding; transcription regulation F;62-112/Domain: myb DNA-binding repeat homology <MYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
                                Ş
                                                                                                                                                                                                                                  C; Function:
                                                                                                                                                                                                                                                    A; Introns:
                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-266 < CON>
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T09744
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                                                                                                                                                                                                                                                                           A;Gene: pl
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anthocyanin biosynthesis regulatory protein Pl - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                        ;62-112/Domain:
                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Zea mays (maize)
Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Superfamily: unassigned myb DNA-binding repeat proteins;
                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                      45/1; 88/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-193 <LOG>
                                                                                               Similarity
  GVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIKRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMSSLGVRKGSWIDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHI
                                    GVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -FDFSNVDTRNFEWVNRFLEVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DASMDNVDP---WWINLLENCND 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHRGASARQGCKFAQQRLVENAKEQVREENTST--GFGESNISFDVDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINNKCGEISTK-----IEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRGNISDQEEDLILRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNSHLSKKVN-----QKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPRE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLKRFDVNKGAWTAEEDRKLAEVITVHGAKRWKTIPSIAGLNRCGKSCRLRWMNYLRPNI
                                                                                                                                                      myb
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                      DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.1%;
                                                                                             26.9%;
                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Mismatches
                                                                                                                                                    repeat
                                                                         Score 397; DB 2;
Pred. No. 6.4e-22;
4; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 400; DB 2;
Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                      homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g2921334
                                                                                                                                                        <MYB1>
                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.; Drummond, B.J.; Tagliani,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myb
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RESULT 15
T01188
Search completed: January 29, 2004, 20:13:20 Job time : 21 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: transcription regulation; stimulates expression of genes involved in anth C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-binding repeat homol C;Keywords: DNA binding; transcription regulation F;9-61/Domain: myb DNA-binding repeat homology <MYB> F;62-112/Domain: myb DNA-binding repeat homology <MYB1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anthocyanin biosynthesis regulatory protein Pl - maize
N;Alternate_names: Pl transcription factor
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A;Introns: 45/1; 88/2
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Cooper, P.S.; Kent, B.; Matz, E.C.; Cone, K.C.
submitted to the EMBL Data Library, July 1997
A;Description: P1-987: a nonfunctional maize anthocyanin regulatory gene resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Molecule type: DNA;Residues: 1-267 <COO>;Residues: 1-267 <COO>;Cross-references: EMBL:AF015268; NID:g2343272; PIDN:AAB67720.1; PID:g2343273;Experimental source: cultivar W22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Reference number: Z14257
;Accession: T01188
;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                         Query Match 26.9%; Score 397; DB 2; Length 267; Best Local Similarity 67.6%; Pred. No. 6.4e-22; Matches 71; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Zea mays (maize)
Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 13-Aug-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: T01188
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                                                                                                                                                                                                                                                                      10 GVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDF 69
                                                                                                                                                       70 EQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK 114
                                                                                                                                                                                                                                       11 GVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIKRGNI 70
                                                                                                                        71 SYDEEDLIVRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNSTLGRR 115
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OM protein - protein search, using sw model on: Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

January 29, 2004, 20:04:26 ; Search time 18 Seconds (without alignments) 715.851 Million cell updates/sec

Title: Perfect score: Sequence: US-10-033-190-2 1477 1 MNSTSMSSLGVRKG

MNSTSMSSLGVRKGSWTDEE.....QQGVQNDDFSAEIDLWNLLD 274

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues

127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33 32 32 32	222222 2276543	17 18 19 20 21 22	9 11 12 13 14 16	878848878	Result No.
167 142.5 137 127.5 108	236.5 236.5 235.5 235.5 185.5		343 39.5 263 262 261.5 255 248.5	411.5 395 394 378 365 363 363	
9.6 9.3 8.6 7.3		16.4 16.3 16.3 16.3	67777733	24.6 24.5	Query Match I
757 811 590 449 595	640 641 382 367 451	751 752 624 640 757 757	421 302 743 704 700 686 728	258 252 273 267 340 399	Length DB
1 CC5_SCHPO 1 BASI_YEAST 1 CEF1_YEAST 1 MYB1_PHYPA 1 REB1_KLULA	L MYB_BOVIN WYB_CHICK WYB_AYIMB L ASLI_ARATH L MYBH_DICDI MYBH_DICDI MYBH_DICDI	I MYBA_MOUSE MYBA_HUMAN I MYB_HUMAN I MYB_HUMAN I MYB_CHICK I MYB_MOUSE	I MYBŽ PHYPA I MYBB TORVU I MYBB TORVI I MYBB MOUSE I MYBB HUMAN I MYBB CHICK I MYB DROME I MYBA XENLA	TT2 ARATH MYBD MAIZE MYBC MAIZE MYBL MORVU MYB1 HORVU MYB1 MAIZE MYB1 MAIZE MYBB MAIZE MYBB MAIZE MYBB MAIZE MYBAIZE	3 ID
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45	44	43	42	41	40	39	38	37	36	35	34
92.5	95.5	95.5	97	98	98	98.5	99	99	99	100	101.5
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P44419	022928	Q01969	P13922	Q51238	P11131	P25588	Q54807	Q53770	P21598	P21538	Q8k9t8
haemophilu	arabidopsi	thermotoga	plasmodium	neisseria n	enterococci	saccharomy	streptococ	staphyloco	enterococcu	saccharomyo	buchnera a

ALIGNMENTS

88888888888888888888888888888888888888	RESULTITIZAR ART RESULTITIZAR ART REN S. S. S. R.
STRAINS-CY COlumbia; MEDLINE-21481677; PubMed=11597504; Stracke R., Werber M., Weisshaar B.; The R2R3-MYB gene family in Arabidopsis thaliana."; Curr. Opin. Plant Biol. 4:447-456(2001). SEQUENCE FROM N.A. STRAINS-CY Columbia; MEDLINE-99087489; PubMed=9872454; MEDLINE-SUBMEDLINE-STRAINEDUS of 1,013,767 bp covered by sixteen physically assigned pl and TAC clones."; "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned pl and TAC clones."; "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned pl and TAC clones."; "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned pl and TAC clones."; "FUNCTION: Transcription factor involved in the control of flavonoid late metabolism in developing siliques. Plays a key role in determining the tissue-specific activation of lewers and inflorescence stems. -!- SUBCELLULARA LOCATION: Nuclear. -!- SIMCLILULAR LOCATION: Nuclear. -!- SIMCLILULAR LOCATION: Supressed at a high level in immature siliques and stemes. -!- DEVELOPMENTAL STAGE: Highly expressed from the very early stages of embryogenesis to the globular stage, decreases rapidly from the late heart-torpedo stage and did not persist after the completion of embryogenesis. -!- SIMCLLAR LOCATION: Transcription of embryogenesis. -!- SIMCLLAR LOCATION: Transcription of embryogenesis. -!- SIMCLLAR LOCATION of the presence	11 ATH ATH ATH ATH PFJA2; 8-FEB-20 8-FEB-20 8-FEB-20 RANSPARE FEB-20 RANSPARE

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RESULT 2
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Best Local Similarity
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VARIANT
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EMBL; AF371981; AAK54744.1; -.
EMBL; AB015477; BAB08716.1; -.
                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Nuclear protein; ATP-bir
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PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
MEDIINE=90151603; PubMed=2303027; Paz-Ares J., Ghosal D., Saedler H.; Paz-Ares J., and the C1-I allele mutant of the regulatory C1 locus."; EMBO J. 9:315-321(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                        SEQUENCE
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01-NOV-1991
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Q -> L (IN CV. WS).
Q -> R: IN TT2-4; LOSS C
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MISSING: IN TT2-2; RED
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P10290;
01-MAR-1989
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28-FEB-2003
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DNA BIND
DOMAIN
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PROSITE; PS00334; MYB-2; 1.
PROSITE; PS00334; MYB-2; 1.
PROSITE; PS50090; MYB-3; 2.
Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                          MAIZE
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                                                                                                                                                                                Spermatophyta; Magnoliophyta; PACCAD clade; Panicoideae; And
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
transcriptional activators.";

EMBO J. 6:3553-3558(1987).

-I- FUNCTION: CONTROLS THE EXPRESSION OF GENES
BIOSYNTHESIS. REGULATES THE EXPRESSION OF A
GENES: CHALCONE SYNTHASE, DIHYROFLAVONOL R
O(3) GLUCOSYLTRANSFERASE. C1 ACTS AS A TRAN
                                                                                  Paz-Ares J., Ghosal D., Wienand U., Peterson P.A., Saedler H.; "The regulatory c1 locus of Zea mays encodes a protein with homology to myb proto-oncogene products and with structural similarities to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activator;
                                                                                 to myb
                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88111545; PubMed=3428265;
                                                                                                                                                                NCBI_TaxID=4577;
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                                                                                                                                                                                                                                                       Anthocyanin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CONTROLS THE EXPRESSION OF GENES INVOLVED IN ANTHOCYANIN BIOSYNTHESIS. REGULATES THE EXPRESSION OF AT LEAST 3 STRUCTURAL GENES: CHALCONE SYNTHASE, DIHYDROFLAVONOL REDUCTASE AND FLAVONOL O(3) GLUCOSYLTRANSFERASE. C1 ACTS AS A TRANS-ACTING FACTOR. SUBCELLULAR ICCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 2 Myb-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X52201; CAA36456.1;
P01103; 1POM.
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                                                                                 proto-oncogene products and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYDEEDLIIRLHRLLGNRWSLIAGRLPGRTENEIKNYWNSTLGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKRGAWTSKEDDALAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIRRGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
252 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                      regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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212
26419
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65.7%;
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                                                                                                                                                                                  Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae; ; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 395; DB 1;
Pred. No. 4.4e-22;
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MYB 2.
POLY-GLY.
, AD61FA2B829C5FBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
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    TRANS-ACTING
               S INVOLVED IN ANTHOCYANIN
AT LEAST 3 STRUCTURAL
REDUCTASE AND FLAVONOL
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This SWI between

SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM

EMBL outstation

a collaboration

SUBCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: Contains 2 Myb-like domains.

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RESULT

MYBLIAN

MYBLIAN

MYBLIAN

MYBLIAN

MYBLIAN

AC P2

AC P3

AC P3

AC P4

AC P4

AC P4

AC P4

AC P4

AC P4

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Best Local S
Matches 69
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Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
SMART; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS00034; MYB 3; 2.
Nuclear protein; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                        Salamini F., Rohde W.;
Salamini F., Rohde W.;
"Multiple genes are transcribed in Hordeum vulgare and Zea mays carry the DNA binding domain of the myb oncoproteins.";
Mol. Gen. Genet. 216:183-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYB1_HORVU
P20026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M37153; AAA33482.1; PIR; S06215; TVZMMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HORVU
                    Wissenbach M., Rohde W.;
                                                                                                                                                                                                                                                               STRAIN=cv. Abyssinian 2231;
MEDLINE=89313655; PubMed=2664447;
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                             STRAIN=cv. Abyssinian 2231; TISSUE=Leaf; MEDLINE=94035190; PubMed=8220488;
                                                                                                                                                                                                                                      Marocco A., Wissenbach M.,
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
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                                                                                                             SEQUENCE FROM N.A.
genes from Hordeum vulgare: tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01103; 1POM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVKRGAWTSKEDDALAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIRRGNI
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205
234
273
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(Rel. 17
(Rel. 40
protein
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                                         Ueberlacker B.,
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17, 1
40, L.
in Hv1.
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65.7%;
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yta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                        Becker D.,
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ASP/GLU-RICH (ACIDIC).
; 163977BBA8CE669D CRC64;
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Pred. No. 5.8e-22;
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                                         Vogt F.,
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                                         Becker D.,
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                                           Salamini
                                                                                                                                                                                                                                          Saedler
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  of.
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                                                                                                                                                                                                                           RESULT 5
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Best Local S
Matches 73
                                                                                                                                                             01-FEB-1991
01-FEB-1991
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
DNA_BIND
SEQUENCE
                                                                                      Spermatophyta; Magnoliophyta;
PACCAD clade; Panicoideae; And
NCBI_TaxID=4577;
                                                                                                                                                                                                    MYB1_MAIZE
P20024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric Myb promoter/Gus genes in transgenic tobacco."; plant J. 4:411-422(1993).
                                MEDLINE=89313655; PubMed=2664447; Marocco A., Wissenbach M., Becker D., Salamini F., Rohde W.;
                                                                                                                                                     Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                              Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T02887; -
InterPro; IPR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
         "Multiple genes are transcribed in Hordeum vulgare and carry the DNA binding domain of the myb oncoproteins.";
                                                                    SEQUENCE FROM N.A.
                                                                                                                                         Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S61506; S61506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOSYNTHESIS.
SUBCELLULAR LOCATION: Nuclear (Probable)
TISSUE SPECIFICITY: GERMINATING SEED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 2 Myb-like domains.
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                                                                                                                                                                                                                                                                           134
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X70879; CAA50224.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01103; 1POM.
                                                                                                                                                                                                                                                                                                                        74
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                                                                                                                                                                                                                                                                                                                                                                      14
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                                                                                                                                                                                                                                                                                                                                                                                                                      73;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                         AASNITISFESAQR 147
                                                                                                                                                                                                                                                                                                                                    EVDLILRLHKILGNRWSLIAGRLFGRTANDVKNYWNTNLLRKLNTTKIVF--REKINNKC 130
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1 (Rel. 17, Last sequ
3 (Rel. 41, Last anno
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62
267 AA;
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                                                                                                                                                                                                                STANDARD;
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112
29740
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                                                                                                     Streptophyta; En
yta; Liliopsida;
; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                sequence up
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MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 378;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activator;
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DBECEDCEBA847749
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                             update)
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IN THE REC
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                                            Paz-Ares
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                                                                                                                                                                 update)
                                                                                                                              Embryophyta; Tracheophyta;
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                                             Saedler
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                      Zea mays
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OF FLAVONOID
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RESULT 6
MYB3 MAISE
ID MYB3 M
AC P20075
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Best Local S
Matches 94
                                                                                                                                        "Multiple genes are transcribed in Hordeum vulc
carry the DNA binding domain of the myb oncopro
Mol. Gen. Genet. 216:183-187(1989).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 2 Myb-like domains.
PIR; $04899; $04899.
HSSP; PO1103; IPOM.
TRANSFAC; T02959; -.
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SMART; SM00717; SANI; ...

PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00034; MYB 2; 1.

PROSITE; PS00090; MYB 3; 2.

Nuclear protein; DNA-Binding; Repeat; Transcription regulation.

Nuclear protein; DNA-Binding; MYB 1.

ONA_BIND 11 63 MYB 1.

ONA_BIND 64 114 MYB 2.

114 T<7319 MW; F2341387F6263DAF CRC64;

Cength 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P20025;
01-FEB-1991
01-FEB-1991
28-FEB-2003
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MaizeDB; 69590;
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Zea mays (Maize)
                              InterPro; IPR001005; Myb_DNA_binding, PF00249; myb_DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marocco A., Wissenbach Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=89313655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S04898; S04898.
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(Rel. 17,
(Rel. 41,
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nbach M., Becker D.,
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annotation update)
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Pred. No. 9.9e-20;
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Best Local
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01-AUG-1992 (Rel
01-AUG-1992 (Rel
28-FEB-2003 (Rel
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DNA_BIND
SEQUENCE
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01-AUG-1992 (Rel. 23, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Myb-related protein P.
          EMBL; M73028; AAA33500.1; -.
EMBL; M73029; AAA33501.1; -.
EMBL; CAA77939.1; -.
                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PARCAD clade; Panicoideae; Andropogoneae; Zea.
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PROSITE; PS50090; MYB_3; 2.
Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                        Genetics 131:199-209(1992).
-!- FUNCTION: TRANSCRIPTION
BIOSYNTHETIC PATHWAY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                    Grotewold E., Athma P., Peterson T.; "Alternatively spliced products of the maize P gene with homology to the DNA-binding domain of myb-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91271238; PubMed=2052542;
                                                                                                    between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The European Bioinformatics Institutions as long use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays (Maize)
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                 transposition
                                                                                                                                                                                                                                                                                                                                            Athma P., Grotewold E., Peterson "Insertional mutagenesis of the r
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92275319;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          factors."
                                                                                                                                                                    IsoId=P27898-2; Sequence=VSP_003301, VSP_003302;
SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                 Name=Short
                                                                                                                                                                                                                           Name=Long;
                                                                                                                                                                                                                                      Event=Alternative
                                                                                                                                                                                                                                                                               FLORAL TISSUES
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62
255 AA;
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                                                                                                                                                                                                                                                                                                                                                                       PubMed=1317315
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112 M
; 27568 MW;
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                                                                                                                                                                                                            Sequence=Displayed;
                                                                                                                                                                                                                                      splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                         FACTOR POSTULATED TO REGULATE THE A FLAVONOID-DERIVED PIGMENT IN CE
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Pred. No. 9.7e
14; Mismatches
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; 26AAADC8B0633E06
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maize
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                                                                            (See http://www.isb-sib.ch/announce,
                                                                                                     There are no rest
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.7e-20
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Best Local
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SMART; SM00717; SANT; 2
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS00396; MYB 3; 2.
Nuclear protein; DNA-binding; Rep.
                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=92034971; PubMed=1934056;
Oppenheimer D.G., Herman P.L., Sivakumaran S., Esch J.,
"A myb gene required for leaf trichome differentiation
is expressed in stipules.";
Cell 67:483-493(1991).
[2]
                                                                                                                                                                                                                                                                                                                                                                             ARATH
                                                                                                                                                                                                                                                                                  GLI ARATH STANDARD; PRT; 228 AA.
PR7900; Q9ST42;
01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Trichome differentiation protein GLI (GLABROUSI protein)
GLI OR ART3G27920 OR KIGN12.7.
           SEQUENCE FI
                                                                                                                                                                                                                                          Arabidopsis thallana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MaizeDB; 69180; -.
MaizeDB; 69181; -.
InterPro; IPRO01005; Myb DNA binding.
                                                                                   Shikazono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                              Shikazono N., Tanaka A., Yok
"Nucleotide sequence of the
ecotype Columbia.";
DNA Seq. 9:177-181(1998).
                                                                                              MEDLINE=99449058; PubMed=10520748;
                                                                                                                      SEQUENCE FROM N.A.
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            FROM N.A.
v. Columbia,
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            Ba-1,
                                                                                   Yokota Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                      cota Y., Watanabe H., Tano S.;
GLABROUS1 gene of Arabidopsis thaliana
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MYB 2.

POLY-ALA.

POLY-LEU.

POLY-LEU.

WSLLASHLPGRTDNEIKNYWNSHLSROIHTYRRKYTAGPDD

WSLLASHLPGRTDNEIKNYWNSHLSROIHTYRRKYTAGPDD

WSLLASHLPGRTDNEIKNYWNSHLSROIHTYRRKYTAGPDD

WSLLASHLPGRTDNEIKNYWNSHLSROIHTYRRKYTAGPDD
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Pred. No. 2e-19;
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/FTId=VSP_003302.
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             CV.
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DNA_BIND
CONFLICT
CONFLICT
SEQUENCE
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00717; SANT; 2.

PROSITE; PS00037; WYB 1; 1.

PROSITE; PS00334; WYB 2; 1.

PROSITE; PS50039; MYB 3; 2.

PROSITE; PS50090; MYB 3; 2.

PROSITE; PS50090; DNA-Dinding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T01588; -.
InterPro; IPR001005; Myb
Pfam; PF00249; myb_DNA-bl
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Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., T
"Structural analysis of Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hauser M.T., Harr B., Schlotterer C.; "Trichome distribution in Arabidopsis thaliana and its close Arabidopsis lyrata: molecular analysis of the candidate gene GLABROUS1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC clones.";
BAC clones.";
Res. 7:217-221(2000).
FUNCTION: REGULATES THE PRODUCTION
FUNCTION: PRECURSOR CELLS ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; AB006078; BAA86879.1; -...

4, AF263690; AAL01215.1; -...

4, AF263693; AAL01218.1; -...

4, AF263694; AAL01219.1; -...

4, AF263695; AAL01220.1; -...

4, AF263697; AAL01221.1; -...

5, AF263697; AAL01221.1; -...

5, AF263697; AAL01221.1; -...

6, AF263697; AAL01221.1; -...

6, AF263697; AAL01221.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                             ISEKOTPDASMDNVDP-----WWINLLENCNDDIEEDEEVVINY
                                                                                                                                              EISTKIEI----
                                                                                                                                                                                                                                                                                            KKGLWTVEEDNILMDYVLNHGTGQWNRIVRKTGLKRCGKSCRLRWMNYLSPNVNKGNFTE
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LAQKDVLMATTN--DPSHYYGNNALWVH-----DDDFELSSLVMMNF
                                                                                             DYSSAVKTTGEDDDSPPSLFITAATPSSCHHQQENIYENIAKSF-NGVVSASYEDKPKQE
                                                                                                                                                                                           QEEDLIIRLHKLLGNRWSLIAKRVPGRTDNQVKNYWNTHLSKKL-----
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228
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149
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C -> R
GDV ->
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Pred. No. 1
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DV -> SDI (IN REF:
822A8646F446F6B9
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we 3. II.
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RESULT 10
MYB3_HORVU
ID MYB3_HORVU
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P80073;
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DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHYPA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01103; 1POM.
TRANSFAC; T02893; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X67050; CAA47435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94004988; PubMed=8401607;
Leech M.J., Kammerer W., Cove D.J.,
"Expression of myb-related genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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DEVELOPMENTAL STAGE: HIGH RATES OF GROWTH.
SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00037; MYB 1; 1.
PS00334; MYB 2; 1.
PS50090; MYB 3; 2.
PXOtein; DNA-Dinding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGD
                                                                                                                               CQSDEGPVLLKVPKAPKSPISVNPGPGCNYDDDSEH---
                                                                                                                                                                              DNVD----
                                                                                                                                                                                                                           EDSKLDDTEDDTDDEGGDSSDVTMSDASKSEKRSKKKSKPKETVKVRQPKGPKPAPQLKM
                                                                                                                                                                                                                                                                        KCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEBEHCKEIISEKQ-----TPDASM
                                                                                                                                                                                                                                                                                                                        FSEAEENLILDLHATLGNRWSRIAAQLPGRTDNEIKNYWNTRLKKRLRSQGLDPNTHLPL
                                                                                                                                                                                                                                                                                                                                                                     FEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKINN
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(Rel.
(Rel.
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         STANDARD;
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112
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                                                                                                                                                                            PWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 343; DB
Pred. No. 5.2e
34; Mismatches
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: 27A3578578D0F3F4 CRC64;
         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin C.,
the moss, F
         302
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.2e-18;
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Physcomitrella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 421;
                                                                                                                                 -SSSSTVTTKSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulation;
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                                                                                                                               238
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Best Local
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01-JUN-1994
16-OCT-2001
                                                                                                                                                     Repeat.
DNA_BIND
DNA_BIND
CONFLICT
                                                                                                                                                                                                      SMART; SM00717; SAÑT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50039; MYB 3; 2.
Nuclear protein; DNA-Ďinding;
                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Multiple genes are transcribed in Hordeum vulgare and carry the DNA binding domain of the myb oncoproteins.", Mol. Gen. Genet. 216:183-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marocco A., Wissenbach M., Becker D., Paz-Ares J., Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric Myb promoter/Gus
Plant J. 4:411-422(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. AbyBsinian 2231; TISSUE=Leaf;
MEDLINE=94035190; PubMed=8220488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myb-related
                                                                                                                                                                                                                                                                                 TRANSFAC; T02889; -. InterPro; IPR001005;
                                                                                                                                                                                                                                                                                                          PIR; S31818; S31818.
HSSP; P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                   EMBL; X70881; CAA50226.1;
EMBL; X70878; CAA50223.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produ
between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Abyssinian 2231;
MEDLINE=89313655; PubMed=2664447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4513;
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                       Pfam; PF00249; myb_DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 35-302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myb genes from Hordeum vulgare: tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wissenbach M., Ueberlacker B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (Probable)
TISSUE SPECIFICITY: GERMINATING SEED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR IN RESPONSE EXTERNAL SIGNAL. MAY BE INVOLVED IN THE REGULATION OF F
              58
                                                                                         67; Conser
NYLRPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNT 117
                                       MGRPSSGAVGQPKVRKGLWSPEEDEKLYNHIIRHGVGCWSSVPRLAALNRCGKSCRLRWI
                                                               MNSTSMSSLG---VRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWL 57
                                                                                                                                          302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                          Conservative
                                                                                                                                                                     641
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114
259
                                                                                                                                           33003
                                                                                                     23.0%;
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yta; Liliopsida; Poales; Poaceae; Pooideae;
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                                                                                          16;
                                                                                                                                                      MYB 1
MYB 2
                                                                                                       Pred.
                                                                                                                  Score 339.5;
                                                                                                                                           A -> P (IN REF. 2).
89017418C3631599 CRC64;
                                                                                                                                                                                                          Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vogt F.,
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                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the myb oncoproteins.";
                                                                                         No. 6.2e-18; smatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions on
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                                                                                                                                                                                                          Transcription regulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
                                                                                                                  Length
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MYBB XENUA ID MYBB X AC P52551 DT 01-OCT DT 30-MAX DT 15-SEP DE MYBL2 OS Xenopu OC Amphib OC Amp
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P52551;
01-OCT-1996
                                                                                                                                                                                                                                    DNA_BIND
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                          Pfam; PF00249; myb_DNA-bInding;
SMART; SM00717; SANT; 3.
PROSITE; PS00037; MYB 1; 3.
PROSITE; PS00334; MYB 2; 3.
PROSITE; PS50090; MYB-3; 3.
PROSITE; PS50090; MYB-3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=92297434; PubMed=1606020;
Bouwmeester T., Guehmann S., El-Baradi T., R
van Wijk I., Moelling K., Pieler T.;
"Molecular cloning, expression and in vitro
characterization of Myb-related proteins in
Mech. Dev. 37:57-68(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
                                                                                                                                                                                                                                                                                                         DNIB_AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M75870; AAC98701.1;
HSSP; Q03237; 1A5J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humbert-Lan G., Pieler T_{\cdot,\cdot} "Regulation of DNA binding activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99214591; PubMed=10187816;
Humbert-Lan G., Pieler T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myb-related protein B
MYBL2 OR BMYB OR MYB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001005; Myb_DNA_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenopus oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ween the SWIBS INSTITUTE. The European Bioinformatics Institute. The by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: PRESENT THROUGHOUT OOGENESIS AND EARLY XENOPUS EMBRYOGENESIS; IN ADULT TISSUE IT IS PRIMARILY DETECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 3 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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  73
                                                83
                                                                                            13
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGIDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem.
  EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIV---
                                              KGPWTKEEDEKVIELVKKYGTKHWTLI-AKQLRGRMGKQCRERWHNHLNPEVKKSSWTEE
                                                                                            KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYLRPDLKRGCFSQQEEDHIVALHQILGNRWSQIASHLPGRTDNEIKNFWNSCIKKKLRQ 120
                                                                                                                                                                                                                             130
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 39, (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 34, Rel. 39,
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus.
                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274:10293-10300(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9, Last sequence update)
2, Last annotation update)
B (B-Myb) (Myb-related pr
                                                                                                                                                                                                                                    82909 MW;
                                                                                                                                                                                         17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                            Nuclear protein;
                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a; Craniata; Vertebrata;
Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                               _binding.
                                                                                                                                                                                                                                                        MYB
MYB
MYB
                                                                                                                                                                Score 263; DB 1;
Pred. No. 7.2e-12;
                                                                                                                                                                                                                                       5FD1D678BB24409B CRC64;
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nuclear transport of B-Myb in .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as its content
                                                                                                                                                                                                                                                                                                                               DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalkbrenner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein 1) (XMYB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         functional
                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                    Length
                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pipidae;
                                                                                                                                                                                         743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
MBL outstation -
                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .ch/announce/
                                                                                                                                        Gaps
  --PR 123
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MYBB_MOISE
MYBB_MOI
P48972;
                                         Phosphorylation.
DNA_BIND 26
DNA_BIND 78
DNA_BIND 130
                                           DNA_BIND
DNA_BIND
DNA_BIND
                                                                                            SMART; SM00717; SANT; 3
PROSITE; PS00037; MYB 1;
PROSITE; PS00334; MYB 2;
PROSITE; PS50090; MYB 3;
          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92366176; PubMed=1501895;
Lam E.W., Robinson C., Watson R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996
                              MOD_RES
                                                                                                                                       InterPro; IPR001005; Myb DNA bip
Pfam; PF00249; myb DNA-binding;
                                                                                                                                                            HSSP; Q03237; 1A5
MGD; MGI:101785;
                                                                                                                                                                        PIR; S33704; S33704.
HSSP; Q03237; 1A5J.
                                                                                                                                                                                             EMBL; X70472; CAA49898.1; EMBL; X73028; CAA51511.1;
                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                  modified
                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                          EMBO
                                                                                                                                                                                                                                                                                                                                                                                    mouse B-myb transcription.";
                                                                                                                                                                                                                                                                                                                                                                                          Lam E.W., Watson R.J.;
"An E2F-binding site mediates cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 7:1885-1890(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-myb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYBL2 OR BMYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myb-related
                                                                                      Franscri
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93327760;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-6 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization and cell
                                                                                                                                                                                                                                                                        ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                   ACTIVITY (BY SIMILARITY).
SIMILARITY: Contains 3 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                        PTM: PHOSPHORYLATED BY CYCLIN PHOSPHORYLATION AT THR-524 IS
                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                            d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         12:2705-2713 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDRIICQAHKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVETGGFLTVKASGQQEER
                                                                                                                                                                                                                                                             non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSESATAIVDSAPEKWMVEYVNFLVPGSDIMESDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKQTPDASMDNVDPWW----INLLENCNDDIEEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKINNKCGEISTKIEIIKPORRKYFSSTM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSGYQAAEDQNHVLLSEPVER---SANIPEEPSNILSPKLLTKSPGIRSEQESGGE-GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 33, (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                              Mybl2
                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8334989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33, Created
            447
                                443
                                         77
129
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (B-Myb) .
                                                                                               ωω
                                                                                                                    ω.
                                                                                                                                                   DNA binding
                                                                                                                                                                                                                                                                                                                                                              Nuclear
                                                                                      Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cycle-regulated
         MYB 1.
MYB 2.
MYB 3.
PHOSPHORYLATION
SIMILARITY).
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                 of Bioinformatics
  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                        A/CDK2 DURING S-PI
PROBABLY INVOLVED
                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
on update)
                                                                                                                                                                                                                                                                                             It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                             regulated
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                                                                                                                                                                                                                                                             as its content
                                                                                    DNA-binding;
                                                                                                                                                                                                                                       http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                                  Usage
            (BY
                                YB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293
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                                                                                                                                                                                                                                                                                 and the
                                CDK2)
            CDK2)
                                                                                                                                                                                                                                                                                                                                                                                             repression
                                                                                                                                                                                                                                                   γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae; Mus.
                                                                                                                                                                                                                                                                        ne EMBL outstation restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTIONAL
            (BY
                                YB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse
                                                                                                                                                                                                                                                                                             a collaboration
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chagman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cligg S., Cobley V.E., Collier R.E., Jeadman R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Pathalingam S.R., Plumb R.W., Ramsay H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYBB_HUI
P10244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                      MEDLINE=21638749;
                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                 Nucleic
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89083548; Pul
Nomura N., Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYBL2 OR BMYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                         "Isolation of human cDNA clones of
                                                                                                                                                                                                                                                                                                                                                                                                            TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199
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                                                                                                                                                                                                                                                                                                 Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                        R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISTKIEIIKPORRKYFSSTMKNVINNNVILDEEEHCKEIISEKOTPDASMDNVDPWWINL
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A., Factalingam
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GO; GO:000 InterPro;

GO:0003700; F:transcription factor erPro; IPR001005; Myb_DNA_binding.m; PF00249; myb_DNA-binding; 3.

MIM;

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Helton E., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
Genew; HGNC:7548; MYBL2.
GK; P10244; -.
                                                                                            EMBL; BC007585; AAH07585;
PIR; S01991; S01991.
HSSP; Q03237; 1A5J.
                                                                                                                                                                                                EMBL; X13293; CF
EMBL; AL121886;
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"Identification of cyclin A/Cdk2 pho
Eur. J. Biochem. 260:384-391(1999).
-i- SUBCELLULAR LOCATION: Nuclear.
-i- PTM: PHOSPHORYLATED BY CYCLIN A/
PHOSPHORYLATION AT THR-520 IS PR
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                                                                 TRANSFAC;
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                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       requires a license agreement
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DNA_BIND 26
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DNA_BIND 130
MOD_RES 444
MOD_RES 447
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MOD_RES 494
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MOD_RES 577
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                  MEDLINE=98322063; PubMed=9657674; McIntosh P.B., Frenkiel T.A., Wollborn U., McKlempnauer K.H., Feeney J., Carr M.D.; "Solution structure of the B-Myb DNA-binding of for conformational instability of the protein control of gene expression."; Biochemistry 37:9619-9629(1998).
                                                                                                                                                                                                                        MEDLINE=93049214; PubMed=1425593; Foos G., Grimm S., Klempnauer K.-H.; Fortinan antagonism between members inhibits v-myb-induced gene activation. EMBO J. 11:4619-4629(1992).
                                                                                                                                                                                STRUCTURE BY NMR OF 79-186
                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
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01-OCT-1993
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(Rel. 41,
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20-MAR-1987 (Re)
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PDB; 1A5J; 01-JUL-yo.
TRANSFAC; T01586; -.
InterPro; IPR001005; Myb DNA bin
PP00249; myb_DNA_binding;
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PROSITE; PS00037; MYB 1; 3.

PROSITE; PS00334; MYB 2; 3.

PROSITE; PS50090; MYB 3; 3.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
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DNA_BIND
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between the Swiss Institute of Bioinformatics and the EMBL
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protein
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TISSUB SPECIFICITY: EXPRESSED IN HEMATOPOIETIC HEMATOPOIETIC CELLS.
SIMILARITY: Contains 3 Myb-1ike domains.
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RX MEDILIBE-2019606; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Mank K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Backer R., Deman B.P., Bandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,
RA Bertis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durker S.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melnet M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Becleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Becleb J.M.,
RA Melson D.R., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., 
                                     use by modified
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                          This
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                                                                                                                                                                                                                                                                                  "Isolation of the proto-oncogene c-myb Cell 41:449-456(1985).

-i- FUNCTION: DNA-BINDING PROTEIN THAT SEQUENCE 5'-YAAC(G/T)G-3'.

-i- SUBCELLULAR LOCATION: Nuclear.
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                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                             SIMILARITY: Contains 3 Myb-like domains.
                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                             pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for con
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                                                                                                                     Q9m715
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                                                                                                                               1 petunia hyb
0 petunia int
9 petunia hyb
7 petunia hyb
8 petunia hyb
6 petunia hyb
2 vitis labru
9 arabidopsis
3 vitis labru
                                                                                              petunia axi
vitis labru
                                                                           petunia axi
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
395.5	396	396	396	396	397	397.	397	397	397	399.5	399.5	400	401	402.5	402.5	403	403	403	403	404	405.5	408	409	415	423.5	428	433	438.5
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184	264	198	181	113	342	271	271	267	266	264	193	193	203	226	226	257	246	226	218	264	388	269	272	302	249	254	247	271
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Q94FG5	Q9ATD1	049017	Q8H262	Q93V39	Q9FJ07	Q8GRW4	Q41842	022450	Q41868	Q9XIU9	Q94FG3	049018	Q9SEI0	Q8H256	049021	Q9S9K9	Q9S7Y2	Q8H255	Q8H253	Q41869	Q40920	Q42379	Q9ZR50	Q9ATD5	Q38850	Q9ATD2	Q9ATD9	Q9ATD3
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ALIGNMENTS

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RESULT 1
Q9M721
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                                                                           HSSP; PUBBOO,
TRANSFAC; T02955; -.
InterPro; IRR01005; Myb DNA binding.
Pfam; PF00249; myb DNA-bInding; 2.
SMART; SM00717; SANT; 2.
SMORTIE; PS00037; MYB_1; 1.
R PROSITE; PS00034; MYB_2; 1.
R PROSITE; PS00334; MYB_2; 1.
R PROSITE; PS00390; MYB_3; 2.
UNA-binding; Nuclear protein.
TOTATEMER 255 AA; 29021 MW; 3C590EE
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=CV. V26; TISSUE=Petal limb;

STRAIN=CV. V26; TISSUE=Petal limb;

(MEDLINE=99380006; PubMed=10449578;

(Quattrocchio F., Wing J., van der Woude K., Souer E.,

Mol J., Koes R.;

I "Molecular analysis of the anthocyanin2 gene of petun
in the evolution of flower color.";

Plant Cell 11:1433-1444(1999).

C -!- SUMCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C -!- SUMCELLULAR LOCATION: ANTH-LIKE DOMAINS.

R EMBL; AF146702; AAF66727.1; -.

R EMBL; AF146702; AAF66727.1; -.

R HSSP; P06876; IMBK.
Query Match
Best Local Similarity
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01-OCT-2000
01-OCT-2000
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4102;
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   47.0%;
53.7%;
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Last annotation update)
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Score 694.5; DB 10; Length 255; Pred. No. 6.2e-47;
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Q9ZTC3 Q9ZTC7 Q9FNV8

Q9fe25

arabidopsis

Q9ztc3

arabidopsis arabidopsis

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Best Local S
Matches 152
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                                                                                                                                                                                                                                                                       InterPro; IPRO01005; Myb DNA_binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SMO0717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS00030; MYB 3; 2.
DNA-binding; Nuclear Protein.
SEQUENCE 255 AA; 29007 MW; 48B18508
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Q9M720;
01-OCT-2000
01-OCT-2000
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AN2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. S9; TISSUE=Petal limb; MEDLINE=99380006; PubMed=10449578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4103;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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                      VP---
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                                                                                  RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKI
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                                                                                                                                                                                                       Conservative
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REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVT-
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Last
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37; Mismatches
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annotation update)
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                    NNNVILDEEEHCKE
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Matches
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Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00090; MYB_3; 2.
DNA-binding; Nuclear Protein.
SEQUENCE 255 AA; 28963 MW; E4628F08
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01-OCT-2000
01-MAR-2003
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Q9M719;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quattrocchio
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                             IGEGNSMQQGQISHENWGEFSLNLPPMQQGVQNDDFSAEI-DLWNLL
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06; PubMed=10449578;
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Pred. No. 5.5
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Matches 100
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PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00334; MYB 2; 1.

PROSITE; PS50090; MYB 3; 2.

DNA-binding; Nuclear protein.

SEQUENCE 127 AA; 14789 MW;
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Q9M718;
01-OCT-2000
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01-MAR-2003
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Q9M717;
01-OCT-2000
01-OCT-2000
01-MAR-2003
Mol J., Koes k.;
"Molecular analysis of the in the evolution of flower
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SEQUENCE FROM N.A.
STRAIN=cv. W22; TISSUE=Petal limb;
STRAIN=q9380006; PubMcd=10449578;
                                                                                                                   STRAIN=cv. W115; TISSUE=Pe
MEDLINE=99380006; PubMed=1
Quattrocchio F., Wing J.,
                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Petal limb;
TISSUE=10449578;
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL; AF146706; AAF66731.1; -.

HSSP; P06876; 1MBK.
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Pred. No. 2.6e-36;
3; Mismatches 8;
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Matches 98
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                                                                                                   InterPro; IPRO01005; Myb DNA_binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT' 2.
SMO0717; SANT' 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 127 AA; 14817 MW; F9285696
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Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00033; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS00034; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 129 AA; 15084 MW; 12D9DD38
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01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                          Quattrocchio F., Wing J., van der Woude Mol J., Koes R.;
"Molecular analysis of the anthocyanin2 in the evolution of flower color.";
Plant Cell 11:1433-1444(1999).
                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-i- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL, AF146707; AAF66732.1; -.
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core
Asteridae; lamiids; Solanales; Solanaceae; Petunia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Cell 11:1433-1444(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF146705; AAF66730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. W44; TISSUE=Petal limb; MEDLINE=99380006; PubMed=10449578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N. STRAIN=CV. W44;
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       37.0%; Sc
78.4%; Pr
tive 15;
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         Score 547; DB
Pred. No. 1.1e
15; Mismatches
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Pred. No. 5.4e-36;
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Best Local S
Matches 121
Q9FNV9
Q9FNV9;
01-MAR-2001
01-MAR-2001
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Q8L5P2;
01-OCT-2002
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"A myb-related gene of the Kyoho grape (Vitis labruscana)
anthocyanin biosynthesis in grapes.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL; AB073012; BAC07539.1;
InterPro; IPR001005; Myb DNA-binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SM0717; SANT; 2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
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PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 247 AA; 28255 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRNK-PLTHSKTKAIKPHPHK-FSKALPRFELKTTAVDTFD-TQVSTSSKPSSTSPQPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPREK 125
                                                                                                                                                                                                                                                                                                                                                          GEFSLNLPPMQQGVQNDDFSAEIDLWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MESLGVRKGAWIQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCRKSCRLRWLNYLKPDIK
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
transcription factor VIMYBA1-2.
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(TrEMBLrel. (TrEMBLrel.
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                                                                                                          PRELIMINARY
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45.3%;
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16,
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Created)
Last seg
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Pred. No. 4.6e-35;
5; Mismatches 80;
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sequence update)
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       RESULT
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Best Local S
Matches 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Khan K., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Khan K., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Khan K., Khaykin E., Khaykin E., Khan K., Kh
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Stracke R., Weisshaar B.;
"MYB transcription factor gene nomenclature in Arabidopsis thaliana.";
"MYB transcription factor gene nomenclature in Arabidopsis thaliana.";
"MYB transcription factor gene nomenclature in Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).
-:- SUBCELULIAR LOCATION: NUCLEAR (BY SIMILARITY)
-:- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AY008378; AAG38380.1; -.
EMBL; AC020665; AAG52158.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Putative transcription factor MYB113 (Myb-related transcription factor, putative).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 246 AA; 28307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001005; Myb_DNA binding Pfam; PF00249; myb_DNA-binding; 2. SMART; SMO0717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
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                                                                                                              183
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLN----TTKIVP 122
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                                                                                                              CNKDEQKDKLININLLDGDNMWWESLLE
                                                                                                                                                                                C-KEIISEKOTPDASMDNVDPWWINLLE
                                                                                                                                                                                                                                                      NKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSIT
                                                                                                                                                                                                                                                                                                                         REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVT--
                                                                                                                                                                                                                                                                                                                                                                                                  GKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKPSIKR
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Pred. No. 5.5e
26; Mismatches
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                                                                                                                                                                                        194
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ches 52;
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246; 21;

Сарв

63

182 167 122

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FOR THE PROPERTY OF STATE OF S
RESULT 10
Q9M715
ID Q9M71
AC Q9M71
AC Q9M71
AC Q9M71
DT 01-OC
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GN AN2 t
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OC Aster
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"A myb-related gene of the Kyoho grape (Vitis labruscana) re
ranthocyanin biosynthesis in grapes.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

REMBL; AB073010; BAC07537.1;

RINETPRO; IPR001005; Myb DNA binding.

REART; SM07017; SANT; 2.

RAST; PS00717; SANT; 2.

RAST; PS00717; SANT; 2.

PROSITE; PS5009; MYB 3; 2.

DNA-binding; Nuclear protein.

SEQUENCE 250 AA; 28597 MW; 9DA7740CE0A99DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9M715;
01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9M715
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                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitac
                                   SEQUENCE FROM N.A.
STRAIN=cv. S1; TISSUE=Petal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myb-related VLMYBAl-1.
                                                                                                                                      NCBI_TaxID=33119;
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MEDLINE=99380006;
                                                                                                                                                                                                                                                                                                    Petunia axillaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-PWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISHENW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRDK-PQTHSKTKAIKPHPHK-FSKALPKFELKTTAVDTFD-TQVSTSSKPSSTSPQPND
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:| : :| : | | : : | | : : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 22, Last sequence update) (TrEMBLrel. 23, Last annotation update) transcription factor VlMYBA1-1.
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                                                                                                                                                                                                                                                                                                                                                                                  protein.
PubMed=10449578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.6%; Score 541; DB 10; Length 2 44.9%; Pred. No. 7.4e-35; tive 37; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
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s labruscana)
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                                                                                        Query Match
Best Local S
Matches 124
                                                                                                                                                                                                                                          STRAIN=CV. Kyoho; TISSUE=Fruit;

Kobayashi S., Ishimaru M., Hiraoka K., Honda C.;

T "A myb_related gene of the Kyoho grape (Vitis labruscana) r

anthocyanin biosynthesis in grapes.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2001) to UCLEAR (BY SIMILARITY).

C -!- SUBCELLULAR IOCATION: NUCLEAR (BY SIMILARITY).

C -!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

R EMBL; AB073013; BAC07540.1; -.

R INTERFOO; IPRO1005; Myb DNA_binding.

R Pfam; PF00249; myb_DNA-binding; 2.

R SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SMO0717; SANT; 2.
PROSITE; PS00033; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 129 AA; 15041 MW; 0E3731FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8L5P1;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=cv. Kyoho;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitis labrusca x Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sanotation update)
Myb-related transcription factor VIMYBA2.
                                                                                                                                                                                PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 307 AA; 34891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8L5P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=105599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLMYBA2
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                                                                                                              Similarity
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                          MSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIK
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MESLGVRKGAWIQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCRKSCRLRWLNYLKPDIK
                                                                                          Conservative
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                                                                                                           36.5%;
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                                                                                          35;
                                                                                        Score 539.5; DB 1
Pred. No. 1.2e-34;
5; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 540;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
edons; core eudicots; Vitaceae;
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s labruscana)
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Best Local :
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                  pfam; PF00249; myb_DNA-binding; 2
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS0030; MYB 3; 2.
DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9M714
Q9M714;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular analysis of the anthocyanin2 in the evolution of flower color."; Plant Cell 11:1433-1444(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SI-: SIMILARITY: CONTAINS 2 MYB-LIKE DOMA EMBL, AF146709; APF66734.1; -.
HSSP; P06876, 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRALIN=cv. S7; TISSUE=Petal limb;
MEDLINE=99380006; PubMed=10449578;
Quattrocchio F., Wing J., van der
Mol J., Koes R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                  DNA-binding; No SEQUENCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=33119;
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InterPro; IPR001005; Myb_DNA_binding.
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RESULT 13 Q9FE25

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Matches 122
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Q9FE25;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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Borevitz J.O., Xia Y., Blount J.,
"Activation Tagging Identifies a
Phenylpropanoid Biosynthesis.";
Plant Cell 12:0-0(2000).
                                                                                                                                                                                                                                                                                                                                     DNA-binding; Nu
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PAP1 OR F25P12.92
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PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
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STRAIN=cv. Columbia-0;
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EMBL; AC009323; AAG09100.1; -.
HSSP; P06876; 1IDY.
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                          SHENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
                                                                                                                                                                                                                           SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
LEES-QEVDILVPEATTTEKGDTLAFDVDQLWSLFD
                                                        ----DVNPPCLGL--NINNVC--DNSIIYNKDKKKDQLVN---
                                                                                 ASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQI
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(TIEMBLrel. 16, Last sequence update)
(TIEMBLEL 23, Last annotation update)
of anthocyanin pigment 1 protein (Putative transcription
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28469 MW;
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Pred. No. 2.2e-34;
0; Mismatches 68;
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WREDLINE=2016519; Pubmed=11130712;

A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

R Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

R Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

R Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

R Kim C.J., Miranda M., Johnson-Hopson C., Khan S., Khaykin B.,

R Kim C.J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

R Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

R Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

R Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

R Machano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

R M. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

R M. Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

R W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                   Query Match
Best Local S
Matches 122
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01-MAR-2003
Putative tra
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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                   PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
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Borevitz J.O., Xia Y., Blount J
"Activation Tagging Identifies
Phenylpropanoid Biosynthesis.";
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-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF062915; AAC83637.1; -.
EMBL; AF325124; AAG42002.1; -.
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                                                                                                                                                                                                                                                DNA-binding; Nuclear
SEQUENCE 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.D.,
                                                                                                                                                   Similarity
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003 (TrEMBLrel. 23, Last annotation update)
transcription factor (Production of anthocyanin pigment
(MYB-related transcription factor, putative, 65699-
                                SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Columbia;
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                                                                                                                      Conservative
                                                                                                                                                                                                                                             ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG52164.1; -.
                                                                                                                                                                                                                                             r protein.
28100 MW;
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                                                                                                                   Score 532.5;
Pred. No. 3.4e
34; Mismatches
                                                                                                                                                                                                                                                309024FD4103700A CRC64;
                                                                                                                   3.4e-34;
ches 76;
                                                                                                                                                                            DB 10;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ZTC7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein SEQUENCE 212 AA; 24508 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001005; Myb DNA binding Pfam; PF00249; Myb DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
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hes 102;
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VILDEEBHCKEIISEKQTPDASMDNVDPWWI: | :::: :: : | |:
                                                                                                                                                                                                                    GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK-------
                                                                                                                                                                                                                                                                          SKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                   SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
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                                                                            DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP----CLGLNINNVCDNS
                                                                                                                                                                              GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKR
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                                                                                                                          LNTTKIVPREK---INNKCGEIST--KIEIIKPQRRKYFSSTMKNVTNNN
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10, Last sequence update)
23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                      Score 524; DB 10;
Pred. No. 1.3e-33;
3; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE53594D17AA02A0 CRC64;
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1 C., Smeeke
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Db 180 IIYNKDKKKDQLVN-----NLIDGDNMWL 203
Search completed: January 29, 2004, 20:12:48
Job time : 43 secs

grandis

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Result
No.
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Maximum DB seq length: 200000000
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 274
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RESULT 1:
ABB81626
ID ABB8
XX ABB8
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XX TOMB
XX 
              Conners K,
                                                                                       29-OCT-2001; 2001WO-US50638
                                                                                                                18-JUL-2002.
                                                                                                                                                                                        Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour.
                                                                                                                                                                                                                                           24-SEP-2002 (first entry)
                                                                                                                                         WO200255658-A2
                                                                                                                                                                 Lycopersicon esculentum.
                                                                                                                                                                                                                  Tomato anthocyanin 1 (ANT1) protein SEQ ID NO:2
                                                                                                                                                                                                                                                                    ABB81626;
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                                       (EXEL-) EXELIXIS PLANT SCI INC.
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                                                                2000US-244685P.
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              Liu A;
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AAM93860
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AAG43305
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AAY58638
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Matches 274
             17-NOV-1999;
17-APR-2000;
22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants
                                                                14-NOV-2000; 2000WO-US31457
                                                                                       25-MAY-2001
                                                                                                                WO200135727-A1
                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                 agricultural biotechnology.
                                                                                                                                                                                                                              Transcription factor; trait modification; seed characteristic; gene therapy;
                                                                                                                                                                                                                                                                   Arabidopsis thaliana transcription factor homologue
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                                                                                                                                                                                                                                                                                                                      AAE01933;
                                                                                                                                                                                                                                                                                                                                             AAE01933 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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N-PSDB; ABQ73046.
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              ; 99US-0166228.
; 2000US-0197899.
; 2000US-0227439.
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Pred. No. 2.4e-262;
Mismatches 0;
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240 240

G2421

Indels Length

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Gaps

60 60

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RESULT 3
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Pineda Ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phrenyl lipid content, to modify fatty acid and modify wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress
                                                                                                                                                                Agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                     plant; transcription factor;
                                                                                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics oplants, e.g. corn, potato and cotton plants -
22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                             Arabidopsis transcription factor #214.
                                                                                                                                                                                                                                                                                                                 AAU93176 standard;
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                                         22-AUG-2001; 2001WO-US26189
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RESULT 4 AAE01932

standard;

Protein;

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31-JUL-2001 AAE01932; AAE01932

(first entry)

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                                                         Query Match
Best Local S
Matches 32
                                                                                                                                                                     homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or annisense nucleic acid, inserting the polynucleotide or annisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower sensecence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 40;
                                                                                                                                                           A. thaliana transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                          are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complements, fragments, or related polynucleotide with 31% to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated or recombinant polynucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK65362
                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilgrim M, Creelman R, Dubell i
Adam L, Ratcliff O, Reuber JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-2001; 2001US-0837944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REUB/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAM/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUBE/)
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JIANG C.
KEDDIE J.
ADAM L.
                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REUBER J L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YU G.
LRLHKILGNRWSLIAGRLPGRTANDVKNYWNT 106
                 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ectopic expression or altered expression of one or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 878-879; 941pp; English.
                                                                                                                              209
                                                           ilarity 100.0%; 1 Conservative 0;
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                                                         Score 32; DB; Pred. No. 3.3
                                                                                            DB 23;
                                                                         3.3e-23;
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                                                                                          Length 209;
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                                                             Indels
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RESULT 5
AAU93177
ID AAU9
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Best Local (
                                                                                                             Matches
AAU93177 standard; Protein; 246 AA
                                                                                                                                                                                              tolerance, seedling vigour, rate. They may also be used transcription factor levels
                                                                                                                                                                                                                                  characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nucritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phremyl lipid content, to modify fatty acid and modify wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress
                                                                                                                                                                                                                                                                                                                    The present sequence is homologue G2422 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reuber
Pineda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription factor; trait structural characteristic; cagricultural biotechnology.
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17-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                               plants, e.g. corn, potato and cotton plants -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REUB/)
(CREE/)
(PILG/)
(RIEC/)
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                                                                                                                                                           Sequence
                                                                                                                                                                                     agricultural biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-335979/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2000;
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                                                                                                                      Local
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RIECHMANN J L.
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CREELMAN R.
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                                                                                                                        Similarity
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                                                            LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
                                                                                    LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
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                                                                                                                                                           246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 99US-0166228.
; 2000US-0197899.
; 2000US-0227439.
                                                                                                             Conservative
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                                                                                                     11.7%; our
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                              , pest and pathogen resistance and germination d in gene therapy. Therefore manipulating s in plants offers great potential in for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental
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Pred. No.
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characteristic; gene therapy;
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22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                        Adam
                                                                                  Pilgrim
                                                                                                                                                                                                                                               (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis transcription factor #215.
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(RATC/)
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                                                                                                                                                                                                                                                                                           (MEND-)
isolated or recombinant polynucleotide
                                          2002-292022/33
                                                                                                                                                           CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
KEDDIE J.
ADAM L.
RATCLIFF O.
REUBER J L.
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                                                                                                                                            REUBER J L.
RIECHMANN J
                                                                                                                                                                                                                                                                                           MENDEL BIOTECHNOLOGY INC
                                                                                                                  PINEDA O
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G
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    Creelman
Ratcliff O,

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                                                         1 R, Dunce, Reuber JL,
                                                          Dubell AJ, Hear
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echmann JL,
 used
                                                                      Jiang C,
L, Yu G,
 ő
                                                                        Keddie J;
Pineda O;
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produce a transgenic

Claim 40; Page 880-881; 941pp; English

cc are a transgenic plant comprising the polynucleotides, a computer creadable medium having stored sequence information, and identifying a commologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a comprising selecting a plant having a complete trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included The invention relates to 1 of 232 isolated or recombinant polynucleotides senescence and

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Matches 32
Specifically, tue, specifically, tue, nlants or seeds, e.g., to nlant of seeds,
                                                                                    Claim
                                                                                                     Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics o plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification). The present sequence is A. thaliana transcription factors.
                                  The present sequence is Arabidopsis thaliana transcription factor The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g. potato and cotton plants, when their expression level is altered.
                                                                                                                                                                                      Reuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agricultural biotechnology.
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(CREE/)
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CREELMAN R.
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                                                                                     Page 70-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                                                                                                          Creelman Heard J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characteristic;
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2000US-0197899.
2000US-0227439.
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                they are used for modifying the nutritional content of ds, e.g., to modify vitamin and mineral content, to mod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor; trait modification;
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3.9e-
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RESULT 7
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XX AAB6
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XX AAB6
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DH 09-J
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KW MYB
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                                                                         The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB90. MYB polypeptides are useful fo enhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, derivatives in a salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a
                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resing a crop in a field -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant; phenylpropanoid biosynthesis.
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                                                             derivatives.
                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Fig 4; 92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF85191.
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Best Local Similarity
Matches 32; Conserv

11.7%; Solidarity 100.0%; If Conservative 0;

Score 32; Pred. No.

DB 22; 3.9e-2

Length 249;

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The invention relates to 1 of 232 isolated or recombinant polynucleotides CC encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered compared to a wild-type or reference plant, or the plant CC phenotype as compared to a wild-type or reference plant, or the plant CC exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that
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N-PSDB; ABK65155.
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16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adam L,
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RATCLIFF O.
REUBER J L.
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DUBELL A J.
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JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M, Creelman
Ratcliff O,
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YU G.
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L, Yu G,
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Pineda O;
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05-JUL-2000;
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                                                                                                                                                                   Borevitz J,
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                                                                                                                                                                                                                                                (SALK )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensitisation;
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                                                                                                                                                                                                                    SALK INST BIOLOGICAL ROBERTS NOBLE FOUND I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000US-0610185.
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215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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Pred. No.
                                                                                                                                                                           Dixon
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New isolated PAP1 or PAP2 gene, useful for increasing pigmentation plants, as reporter genes for analysing expression pattern of promof interest, and to increase flux through phenylpropanoid pathway

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Claim

9; Page 28;

29pp;

English.

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RESULT 10
AAE30046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription factor; metabolite pathway; terpenoid; limonene synthase; alkaloid pathway gene; taxadiene synthase; biological pathway; freezing; abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress; abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress; abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress; cold; drought; drought; heat; nutrient deficiency; biotic stress; cold; drought;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental significance. The present sequence represents the A. thaliana PAP2
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Determining whether one of several test transcription factor polynucleotides encodes pathway TF by determining expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE30046 standard; Protein; 249 AA
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                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis
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                                                                                                                                                                                                                                                         (MEND-) MENDEL BIOTECHNOLOGY INC
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                                                                                                 AAD47497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway gene; taxadiene synthase; b:
stress; cold; drought; heat; nutrient
n; developmental_pathway; flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
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                                                                                                                                                                                                                                                                                                                                                                                 2002WO-US07999
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3.9e-23;
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It is also useful for identifying one or more transcription factors that activate one or more genes of a biological pathway of a plant, fungi or animal cell, where the biological pathway can be a biochemical pathway such as biosynthetic pathways for soluble and insoluble carbohydrates, for amino acids and a response pathway to abiotic stress such as cold, freezing, drought, heat, nutrient deficiency, pH or biotic stress such as fungal, viral or bacterial infection, developmental pathway such as flowering, root development, a response pathway to environmental cues such as light intensity and light quality, circadian rhythm. Sequences of the invention are used to generate transgenic plants. The present sequence is Arabidopsis thaliana G663 transcription factor protein.
                                                                                                                                                                                                                                                                                                                                                                              polynucleotides encodes a biosynthetic pathway transcription factor or a primary metabolite pathway gene or a secondary metabolite pathway gene such as a terpenoid or alkaloid pathway gene transcription factor. It is also useful for determining whether a member of a pool of test encodes a Mentha sp. or Taxus sp. terpenoid pathway gene where the terpenoid pathway gene encodes limonene synthase (LS) or taxadiene synthase (TDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway gene promoter linked to reporter gene in a cell in presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of one or more genes in a pathway. The method is useful for determining whether a member of a pool of test transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a high-throughput method for identifying a polynucleotide which encodes a transcription factor for controlling the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides
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Matches 32
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100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; 1
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Sequence

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Length 249;

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RESULT 12
AAU93155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB90. MYB polypeptides are useful foenhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, flavonoids, lignins, salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                       microbial disease resistance; herbicide resistance; seed yiel fruit yield; growth rate; leaf senescence; flower senescence. plant; transcription factor; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resi a crop in a field -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Fig 3B; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-316365/33.
N-PSDB; AAF85190.
                                                                                                                          22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
                                                                                                                                                                                                                                                                                                                 Arabidopsis
                                                                                                                                                                                                                                                                                                                                         02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                AAU93155
                                                                                                                                                                                                                                                                                                                                                                                      AAU93155 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                 (HEAR/)
                                                                 (MEND-)
(PILG/)
(CREE/)
                                                                                                                                                                22-AUG-2001; 2001WO-US26189.
                                                                                                                                                                                       28-FEB-2002.
                                                                                                                                                                                                           WO200215675-A1
                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                           Agriculture; metabolic chemical; environmental stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2000;
          (ADAM/)
                                                                                                                 16-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BADI )
                                                        (DUBE/)
                       KEDD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
KEDDIE J. .
ADAM L.
RATCLIFF O.
                                CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ü
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                          MENDEL BIOTECHNOLOGY
                                                                                PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGNRWSLIAGRIPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                  transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                 2000US-0713994.
2001US-0837944.
                                                                                                                                                                                                                                                                                                                                        (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.9%;
                                                                                                                                                                                                                                                                                                                  factor #193
                                                                                                                                                                                                                                                                                                                                                                                       212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                 se; drought;
seed yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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controlled sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynuclectide is used for producing a plant having a modified trait, the method comprising selecting a polynuclectide that encodes a polypeptide or an antisense nucleic acid, inserting the polynuclectide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial classes resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                                                                                                                                                                                                                                       encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to 1 of 232 isolated or recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated or recombinant polynucleotide
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(RIEC/)
(YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-292022/33.
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PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REUBER J L.
RIECHMANN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                     transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 794-795; 941pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dubell AJ, new_
TL, Riechmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heard J,
echmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              produce
                                                          proteins which are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e J;
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밁 á Query Match Best Local ( Matches Sequence 83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109 |||||||||||||||||||||| 80 LLGNRWSLIAGRLPGRTANDVKNYWNT 106 . Similarity 27; Conserv Conservative 9.9%; o ; Score 27; Pred. No. Mismatches DB 23 0 Length Indels 0 Gaps 0

212

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RESULT 13
AAU75734
ID AAU75
XX AAU75
XX AAU75
XX 08-MA
DT 08-MA
XX PAP1;
KW trans
XX Stree
XX Arabi
XX WO2000
                                                                                                                    A. thaliana Production of anthocyanin pigment 1 (PAP1)
                                                                                                                                            08-MAY-2002
                                                                                                                                                                                          AAU75734 standard; Protein; 248
                                                                                                                                            (first entry)
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protein

PAP1; production of anthocyanin pigment; MYB-like transcription factor; transgenic; plant; phenylpropanoid; stress; light stress; water stress; pH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration; sensitisation; chromosome 1.

Arabidopsis thaliana

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AAB82483
ID AAB8
XX
AC AAB8
AC AAB8
XX
DT 22-J
XX
XX
Cotl
XX
XX
Cotl
X
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour expression. The nucleotide sequence is also useful for enhancing accumulation of phenylpropanoid product in a plant. A transgenic plant is useful for detecting a stress condition such as light stress water stress on a stress condition such as light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stress, water stress, pH stress, temperature stress, heavy metal stress, pathogen attack or infection, wounding, nutrient deficiency, herbivory, or abnormal hormone levels in a plant. PAPI or PAP2 overexpression can also be useful in developing or enhancing desirable colouration in ornamental plants for commercial sales, and for sensitising plants to stress. Introduction of PAPI or PAP2 sensitises sensitising plants to stress. Introduction of PAPI or PAP2 sensitises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to the nucleotide and protein sequences of novel Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromosome 1. PAP1 and PAP2 are MYB-like transcription factors that regulate the production of anthocyanin pigment. The nucleotide sequence of the invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for PaP1 are the legitary transferred to the contract of the contract 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental significance. The present sequence represents the A. thaliana PAP1 protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated PAP1 or PAP2 gene, useful for increasing pigmentation plants, as reporter genes for analysing expression pattern of promo of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                  Cotton transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2000;
05-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002
                                      WO200140250-A1
                                                                                                                   Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB82483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB82483 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borevitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-164443/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALK INST BIOLOGICAL STUDIES.
ROBERTS NOBLE FOUND INC SAMMUEL.
                                                                                                                                                                                                    MYB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0603244.
2000US-0610185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US19734.
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                cotton; transcription factor; transgenic plant.
                                                                                                                       CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; **
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                                                                                                                                                                                                                                                                                  factor GhMYB
                                                                                                                       Acala SJ-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 23; L; Pred. No. 3.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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RESULT 15
AAB33327
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription in a plant involves introducing into the plant a recombinant expression cassette comprising a promoter that is operably linked to a heterologous polynucleotide encoding a MYB protein, especially GhMYB 1 or GhMYB 6. The plant is especially a cotton plant, and the promoter directs expression of the polynucleotide in cotton fibres or rects expression be conferred on the plant by this method, e.g. increased fibre quality, yield, length, strength or fineness, alteration of root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating transcription in plants for improving cotton fiber quality, comprises introducing a recombinant expression cassette comprising a promoter operably linked to a sequence encoding a MYB polypeptide -
                                                                                                                                                                                                          Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogamy; bZI; G-box binding factor; basic helix-loop-helix zipper; homeodomin; homeodox; MADS; homeodomain; transcripter; LIM domain; AP2; EREBs; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1999;
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                                          11-MAR-1999;
18-AUG-1999;
                                                                                   09-MAR-2000; 2000WO-US06112
                                                                                                              14-SEP-2000
                                                                                                                                     WO200053724-A2.
                                                                                                                                                                   Eucalyptus grandis.
                                                                                                                                                                                                                                                                              Eucalyptus grandis transcription factor protein sequence #423
                                                                                                                                                                                                                                                                                                             25-JAN-2001
                                                                                                                                                                                                                                                                                                                                       AAB33327;
                                                                                                                                                                                                                                                                                                                                                                   AAB33327 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             architecture, and enhanced growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pre-anthesis fibre cDNA library. A claimed method of modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor GhMYB 7. The sequence was deduced from GhMYB 7 clisolated from a Gossypium hirsutum cv. Acala SJ-2 10-day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of cotton R2R3-MYB transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2000;
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(GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-397938/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 LHKLLGNRWSLIAGRLPGRT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                       81 LHKLLGNRWSLIAGRLPGRT 100
                                                                                                                                                                                              cys2His2; CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                 Query Match 6.2
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                                                                                                                                                                                                                                                        The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: ball, ball, ball, family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 726; 747pp; English.
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                                                                       McGrath A,
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|                                                                                                                                                                                                                                                                                                           | <b>๑๑๑๑๑๑๑๑</b> ๑                                                                                                                                                                                                                                                                                                                    | <b>,</b> , , , , , , , , , , , , , , , , , ,                                                                                                                                                                                                                        | <b>ਗ਼ ਗ਼ </b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | , o o o o o o o o                                                                                                                                                                                                                                                                                                                  |
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| equence 2, Appl<br>equence 2, Appl<br>equence 31262,<br>equence 3092,<br>equence 20195,<br>equence 20195, A<br>equence 783, A<br>equence 783, A<br>equence 3, Appl<br>equence 202, Appl<br>equence 197, Ap                                                                                                | quence 155, Ap<br>quence 4141, A<br>quence 31701,<br>quence 16975,<br>quence 26948,<br>quence 22506,<br>quence 205971,<br>quence 29871,                                                                                                                                                                                              | equence 25699, equence 27508, equence 277, App equence 27, App equence 41, App equence 414, App                                 | equence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | quence<br>quence<br>quence<br>quence<br>quence<br>quence<br>quence<br>quence                                                                                                                                                                                                                                                       |
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|                                                                                                                                                                                                                                                                                                           | <b>ຑຑຑຑຑຑຑ</b> ຑ                                                                                                                                                                                                                                                                                                                     | <b>ຑຑຑຑຑຑຑຑຑ</b> ຑຑ                                                                                                                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | n                                                                                                                                                                                                                                                                                                                                  |
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| JS-08-482-142-120<br>JS-08-493-235-20<br>JS-08-478-727-120<br>JS-08-484-296-120<br>JS-09-911-927-35<br>JS-09-911-882-35<br>JS-09-911-888-35<br>JS-08-146-028-73<br>JS-08-123-422A-73<br>JS-09-112-06-73                                                   | -728<br>-728<br>-728<br>-728                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 15-08-198-151<br>15-08-189-131-180<br>15-08-471-068-180<br>15-08-905-223-382<br>15-09-645-470-21<br>15-09-645-470-27<br>15-09-645-470-27<br>15-09-645-470-27<br>15-09-645-470-27                                                                                                       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18-08-469-615-11 18-08-469-615-11 18-08-469-615-11 18-08-489-615-11 18-08-489-615-11 18-08-489-615-11 18-08-489-615-11                                                                                                                                                                                                                                                                                                               | US-08-199-776-21 US-08-482-142-9 US-07-952-853-20 US-08-478-572-9 US-08-632-731-21 US-08-663-731-21 US-08-663-731-21 US-08-663-731-21 US-08-602-999A-114 US-08-602-999A-114 US-09-736-447-1185 US-09-736-457-1856 US-09-319-570A-5 US-08-306-871-44 US-08-306-871-44 US-08-509-959-44 US-08-085-959-44 US-08-085-959-44 US-08-085-737-7 US-08-075-520A-37 |
| 120,<br>120,<br>120,<br>120,<br>120,<br>120,<br>120,<br>120,                                                                                                                                                                                              | 228,<br>228,<br>228,<br>228,                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 180<br>180<br>180<br>180<br>382<br>382<br>27,<br>27,<br>27,                                                                                                                                                                                                                            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Sequence 7, Appli Sequence 11, Appli Sequence 7, Appli                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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|                                                                                                                                                                                                                                                           | 096<br>090<br>190<br>190<br>190<br>190<br>190<br>190<br>190<br>190<br>190                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                        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| 675<br>676<br>677<br>678<br>680<br>681<br>682                                                                                                                                                                                                             | pp1 668 pp1 669 pp1 670 pp1 671 pp1 672 pp1 673 pp1 673                                                                                                                                                                                                                                                                                                                                                                                                                           | 6 6 6 5 4 6 5 6 5 6 5 6 5 6 5 6 5 6 5 6                                                                                                                                                                                                                                                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635<br>637<br>637<br>637<br>638<br>639<br>640<br>641<br>641<br>642<br>5<br>643<br>5<br>643<br>5<br>7<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8                                                                                                                                                                                                                                                                                                                                                                                                                  | 613 5 1.8<br>614 5 1.8<br>615 5 1.8<br>617 5 1.8<br>618 620 5 1.8<br>620 5 1.8<br>622 5 5 1.8<br>623 5 1.8<br>625 5 1.8<br>626 5 1.8<br>631 5 1.8<br>633 5 1.8<br>633 5 1.8                                                                                                                                                                                                                                            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| 675 5 1.8 35<br>676 5 1.8 36<br>677 5 1.8 36<br>678 5 1.8 36<br>680 5 1.8 36<br>681 5 1.8 36<br>682 5 1.8 36<br>683 5 1.8 36                                                                                                                              | pp1 668 5 1.8 35 pp1 669 5 1.8 35 pp1 670 5 1.8 35 pp1 671 5 1.8 35 pp1 672 5 1.8 35 pp1 673 5 1.8 35 pp1 673 5 1.8 35 pp1 673 5 1.8 35                                                                                                                                                                                                                                                                                                                                           | 660 5 1.8 34 662 5 1.8 34 663 5 1.8 34 665 5 1.8 34 665 5 1.8 34 665 65 5 1.8 34 34 35 65 65 65 65 65 65 65 65 65 65 65 65 65                                                                                                                                                          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635<br>636<br>637<br>638<br>639<br>51.8<br>32<br>640<br>51.8<br>32<br>641<br>51.8<br>32<br>642<br>51.8<br>32<br>644<br>51.8<br>32<br>645<br>51.8<br>32<br>645<br>51.8<br>32<br>646<br>51.8<br>32<br>647<br>51.8<br>32<br>648<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>51.8<br>32<br>649<br>649<br>51.8<br>32<br>649<br>649<br>649<br>649<br>649<br>649<br>649<br>649 | 613<br>614<br>616<br>616<br>617<br>618<br>619<br>620<br>621<br>622<br>623<br>623<br>623<br>623<br>623<br>623<br>623<br>623<br>633<br>63                                                                                                                                                                                                                                                                                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| 675 5 1.8 35 4 US-08-649 676 5 1.8 36 2 US-08-146 677 5 1.8 36 2 US-08-154 678 5 1.8 36 3 US-08-554 679 5 1.8 36 3 US-08-723 680 5 1.8 36 3 US-08-723 681 5 1.8 36 3 US-09-112 682 5 1.8 36 3 US-09-112 683 5 1.8 36 3 US-09-112 684 5 1.8 40 3 US-08-973 | pp1     667     5     1.8     35     2     US-08-478       pp1     668     5     1.8     35     2     US-08-337       pp1     669     5     1.8     35     2     US-08-478       pp1     671     5     1.8     35     3     US-08-478       pp1     671     5     1.8     35     3     US-08-483       pp1     673     5     1.8     35     3     US-08-697       pp1     673     5     1.8     35     3     US-08-637       096     674     5     1.8     35     4     US-08-637 | 559 5 1.8 34 2 US-08-449 5 660 5 1.8 34 2 US-08-184 662 5 1.8 34 2 US-08-184 663 5 1.8 34 2 US-08-184 663 5 1.8 34 2 US-08-521 664 5 1.8 34 2 US-08-521 665 5 1.8 34 3 US-09-239 665 5 1.8 34 3 US-09-239 665 5 1.8 34 3 US-09-239 665 5 1.8 34 3 US-08-487 667 5 1.8 35 1 US-08-487                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 650 5 1.8 34 1 US-08-443 651 5 1.8 34 1 US-08-443 652 5 1.8 34 1 US-08-449 653 5 1.8 34 1 US-08-449 655 5 1.8 34 1 US-08-449 655 5 1.8 34 1 US-08-449 655 6 5 1.8 34 2 US-08-477 657 5 1.8 34 2 US-08-477 658 5 1.8 34 2 US-08-477 658 5 1.8 34 2 US-08-479 658 5 1.8 34 2 US-08-479 658 5 1.8 34 2 US-08-479 658 6 1.8 34 2 US-08-449 6 1.8 34 2 U | 635 5 1.8 32 1 US-09 636 5 1.8 32 1 US-09 637 5 1.8 32 1 US-08 639 5 1.8 32 1 US-08 640 5 1.8 32 1 US-08 641 5 1.8 32 1 US-08 642 5 1.8 32 1 US-08 643 5 1.8 32 1 US-08 644 5 1.8 32 1 US-09 645 5 1.8 32 4 US-09 646 5 1.8 33 1 US-08 647 5 1.8 33 1 US-08 648 5 1.8 33 1 US-08 649 5 1.8 33 1 US-08                                                                                                                                                                                                                                                                                                           | 613 5 1.8 26 4 US-09-227 614 5 1.8 26 4 US-09-215 615 5 1.8 27 6 5466783-2 616 5 1.8 27 6 5498694-8 617 5 1.8 28 2 US-08-482 619 5 1.8 28 3 US-09-040 620 5 1.8 28 4 US-09-040 621 5 1.8 28 4 US-09-027 622 5 1.8 28 4 US-09-225 623 5 1.8 28 4 US-09-205 624 5 1.8 30 1 US-08-08-18 625 5 1.8 30 1 US-08-08-18 626 5 1.8 30 1 US-08-08-18 627 5 1.8 30 1 US-08-08-18 628 5 1.8 30 4 US-09-056 630 5 1.8 30 4 US-09-056 631 5 1.8 30 6 5177189-072 632 5 1.8 30 6 5177189-072 633 5 1.8 30 6 5177189-072                                                |

|                                                                                                                                                                                                                  | 739<br>740<br>741<br>742<br>743<br>744<br>746<br>746                                                                                                                                      | 7736                                                                                                                                                                                                                                             | 709 710 711 712 713 714 715 716 717 717 717 717 717 717 717 717 717                                                                                                                                                                                                                                                                                                                                                    | 686<br>686<br>688<br>688<br>689<br>689<br>689<br>689<br>699<br>699                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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| ហហហហហហហហហ                                                                                                                                                                                                        | n ហ ហ ហ ហ ហ ហ ហ ហ                                                                                                                                                                         | ហហហហហហហហហហហ                                                                                                                                                                                                                                      | ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ                                                                                                                                                                                                                                                                                                                                                                                  | ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| 0 0 0 1 0 U U U U U                                                                                                                                                                                              |                                                                                                                                                                                           |                                                                                                                                                                                                                                                  | @ @ @ @ @ Q J J J J J J J J J J J J J J                                                                                                                                                                                                                                                                                                                                                                                | 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| IS-08-679-338-4 IS-09-293-238B-4 IS-08-675-499A-8 IS-08-675-499A-7 IS-09-482-273-146 IS-09-482-273-125 IS-09-482-07813-25 IS-09-108-01-089-10 IS-09-20-085-305-21                                                | IS-09-912-962-16 IS-09-912-962-17 IS-09-912-962-18 IS-08-519-103-15 IS-08-905-223-489 IS-08-018-635-15 IS-09-018-635-15 IS-09-912-962-15 IS-09-912-962-15 IS-08-199-776-4 IS-08-139-731-4 | 168045-6<br>168045-6<br>19-07-800-364B-8<br>18-07-800-364B-8<br>18-08-685-871-64<br>18-08-519-103-16<br>18-08-519-103-17<br>18-08-519-103-17<br>18-08-519-103-17<br>18-08-519-103-17<br>18-08-519-103-17<br>18-08-519-103-17<br>18-09-018-635-17 | S-08-062-472B-24 S-08-637-759B-236 S-08-800-644-102 S-08-800-644-106 S-08-801-355A-236 S-09-201-345-236 S-09-207-345-236 S-09-227-357-345 S-09-227-357-345 S-08-427-616-10 S-08-446-648-10 S-08-446-648-10 S-08-469-537A-62 S-08-469-537A-63 | US-08-990-888-7 US-08-865-773-8 US-08-865-773-9 US-08-981-189B-4 US-08-981-189B-5 US-09-400-716-6 US-09-400-716-7 US-09-424-127-9 5177060-6 5177060-6 5177060-7 US-08-20-599-1 US-08-766-858A-31 US-08-499-676A-29 US-08-499-676A-30 US-08-499-676A-31 5185440-6 US-08-96-676A-31 5185440-6 US-08-96-676A-31 US-08-99-676A-31 US-08-99-676A-31 US-08-499-676A-31 US-08-499-676A-31 US-08-499-676A-31 US-08-499-676A-31 US-08-499-676A-31 US-08-499-676A-31 US-08-95-676A-31 US-08-95-676A-31 US-08-95-676A-31 US-08-95-676A-30 US-08-95-676A-31 |
| Sequence 4, Appli<br>Sequence 8, Appli<br>Sequence 8, Appli<br>Sequence 30, Appli<br>Sequence 4, Appli<br>Sequence 146, Appl<br>Sequence 15, Appl<br>Sequence 16, Appl<br>Sequence 10, Appl<br>Sequence 21, Appl |                                                                                                                                                                                           |                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|                                                                                                                                                                                                                  |                                                                                                                                                                                           | - Marie Land                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 824<br>824<br>824<br>826<br>827<br>828<br>828                                                                                                                                                                    | 812<br>813<br>814<br>816<br>816<br>818<br>819<br>819                                                                                                                                      | 800<br>800<br>800<br>800<br>800<br>800<br>800<br>810                                                                                                                                                                                             | 782<br>782<br>783<br>785<br>786<br>799<br>799<br>799<br>799                                                                                                                                                                                                                                                                                                                                                            | 758<br>759<br>760<br>760<br>760<br>760<br>760<br>770<br>770<br>770<br>770<br>770                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                                                                                                                  |                                                                                                                                                                                           | 88888888888888888888888888888888888888                                                                                                                                                                                                           |                                                                                                                                                                                                                                                                                                                                                                                                                        | 758 759 760 760 760 762 762 763 764 766 766 767 770 770 771 771 771 771 771 771 771 77                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| 5 1.8 85 4<br>5 1.8 85 4<br>5 1.8 85 4<br>5 1.8 86 3<br>5 1.8 86 3<br>1.8 86 3<br>1.8 86 3<br>1.8 87 3                                                                                                           | 5 1.8 79 4 5 1.8 81 4 5 1.8 82 4 5 1.8 83 2 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                         | 5 1.8 76 4<br>5 1.8 76 4<br>5 1.8 76 4<br>5 1.8 77 4<br>5 1.8 77 4<br>5 1.8 77 4<br>7 1.8 77 4<br>7 1.8 78 3                                                                                                                                     | 5 1.8 67 4 5 1.8 68 1 5 1.8 68 1 5 1.8 68 2 5 1.8 68 2 7 1.8 68 2 7 1.8 69 5 7 1.8 7 1 7 1 1 7 1 4 7 1 4 7 1 4                                                                                                                                                                                                                                                                                                         | 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 5 1.8 85 4<br>5 1.8 85 4<br>5 1.8 85 4<br>5 1.8 86 3<br>5 1.8 86 3<br>1.8 86 3<br>1.8 86 3<br>1.8 87 3                                                                                                           | 5 1.8 79 4 5 1.8 81 4 5 1.8 82 4 5 1.8 83 2 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                         | 5 1.8 76 4<br>5 1.8 76 4<br>5 1.8 76 4<br>5 1.8 77 4<br>5 1.8 77 4<br>5 1.8 77 4<br>7 1.8 77 4<br>7 1.8 78 3                                                                                                                                     | 5 1.8 67 4 5 1.8 68 1 5 1.8 68 1 5 1.8 68 2 5 1.8 68 2 7 1.8 68 2 7 1.8 69 5 7 1.8 7 1 7 1 1 7 1 4 7 1 4 7 1 4                                                                                                                                                                                                                                                                                                         | 5 5 1 1 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

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| 999988888<br>9999<br>9001<br>9002                                                                                                                                 | 890<br>891<br>893<br>893                                                                                                   | 8885<br>887<br>887                                                               | 883<br>884                                                              | 877<br>878<br>879                                                                                                             | 873<br>874<br>875                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 870<br>871<br>872                                                                              | 866<br>867<br>868<br>869                                                             | 863<br>864<br>865                                                                | 859<br>860<br>861                                                                            | 855<br>855<br>857                                                                                | 852<br>853<br>854                                           | 849<br>850<br>851                                           | 846<br>847<br>848                                           | 8 8 8<br>4 4 4<br>5 4 5                                       | 841<br>842<br>843                         | 838<br>839<br>840                                              | 836<br>837                                                     | 831<br>832<br>833<br>834                                                     |
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| ហហហហហហហហហ                                                                                                                                                         | រហហហហហហ                                                                                                                    | ា ហ ហ ហ ហ ហ                                                                      | ហហហហហ                                                                   | ហេហហប                                                                                                                         | ភហ់ហហ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ហ្ហេហ                                                                                          | ហហហហ                                                                                 | ហហហហ                                                                             | ហហហប                                                                                         | រយេយ                                                                                             | ហហហ                                                         | ຫ ຫ ຫ                                                       | ហហហ                                                         | ហេហ                                                           | <b>ภ</b> ဟ ဟ                              | տտտ                                                            | տտտ                                                            | ហេហហហ                                                                        |
| 111111111                                                                                                                                                         |                                                                                                                            |                                                                                  |                                                                         |                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                | 11.88<br>8888                                                                        |                                                                                  |                                                                                              |                                                                                                  |                                                             |                                                             |                                                             | 1.8                                                           | 1.8                                       | <br>                                                           | 1.88                                                           | 1.88                                                                         |
| 107<br>107<br>107<br>107<br>107<br>107<br>107                                                                                                                     | 000000                                                                                                                     | 105                                                                              | 00000                                                                   | 0000                                                                                                                          | 0000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 9 9 9                                                                                          | 97<br>98<br>98                                                                       | 97<br>97<br>97                                                                   | 966                                                                                          | 0 9 9 9<br>5 5 5 5                                                                               | 93<br>94<br>95                                              | 92<br>93                                                    | 91<br>92<br>92                                              | 90<br>91                                                      | 999                                       | 90<br>90                                                       | 90 88                                                          | 87<br>88<br>88                                                               |
| ט ט ט ט ט ט ט 4 4 4                                                                                                                                               |                                                                                                                            |                                                                                  |                                                                         |                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                |                                                                                      |                                                                                  |                                                                                              |                                                                                                  |                                                             |                                                             |                                                             |                                                               |                                           |                                                                |                                                                |                                                                              |
| US-08-480-070C-16 US-08-699-525-16 US-08-609-583A-16 US-09-102-528-27 US-09-102-528-27 US-09-317-399-16 US-09-313-337-16 US-09-464-231-16                         | 9-083-352-8<br>9-083-352-20<br>9-252-991A-3<br>8-487-748A-1<br>8-417-460-12<br>8-398-633-16                                | 9-139-<br>9-732-<br>9-083-<br>9-083-                                             | 9-482-2/3-1<br>8-858-207A-<br>9-205-258-1<br>9-252-991A-<br>9-187-789-2 | 9-128-<br>9-496-<br>8-180-                                                                                                    | 8-282-951-2<br>8-478-097A-<br>8-931-858E-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 8-014-153D-<br>8-974-549A-<br>9-107-532A-                                                      | 9-422-936-83<br>8-851-843A-1<br>8-854-050-12<br>9-430-323-12                         | 8~602-010A-2<br>8-680-726A-2<br>9-092-409-22<br>9-422-936-73                     | 9-736-457-1<br>9-736-457-1<br>9-252-991A-<br>9-403-343B-                                     | 9-047-125-34<br>7-736-335E-34<br>9-134-001C-49                                                   | 835-26<br>8-814-030-1<br>7-987-272A-9                       | 9-252-9<br>9-134-(<br>9-615-)                               | 9-390-1348-3<br>9-047-125-13<br>7-736-335E-1                | 9-107-532A-720<br>8-858-207A-396                              | 9-198-452A-<br>9-107-532A-<br>9-107-532A- | 9-334-601-2<br>9-334-601-2<br>9-334-601-2                      | 9-732-210-1<br>9-252-991A-<br>9-085-305-2                      | 9-107-532A-55<br>8-576-626A-43<br>8-858-207A-50<br>9-222-938A-1              |
| Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 23, Appl Sequence 27, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl |                                                                                                                            |                                                                                  |                                                                         |                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                |                                                                                      |                                                                                  |                                                                                              |                                                                                                  |                                                             |                                                             |                                                             |                                                               |                                           |                                                                |                                                                | 550<br>43,<br>504                                                            |
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| 968<br>970<br>971<br>972<br>973<br>974<br>975                                                                                                                     | 963<br>963<br>965<br>967                                                                                                   | 959<br>960<br>961                                                                | 955<br>957                                                              | 949<br>950<br>952                                                                                                             | 946<br>947<br>948                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 943<br>944<br>945                                                                              | 939<br>940<br>941<br>942                                                             | 935<br>936<br>937<br>938                                                         | 932<br>933<br>934                                                                            | 928<br>929<br>930                                                                                | 925<br>926<br>927                                           | 922<br>923<br>924                                           | 919<br>920<br>921                                           | 917<br>918                                                    | 914<br>915                                | 911<br>912<br>913                                              | 910<br>909<br>908                                              | 904<br>905<br>907                                                            |
| 968<br>969<br>970<br>971<br>972<br>5<br>973<br>5<br>974<br>5<br>976                                                                                               |                                                                                                                            |                                                                                  |                                                                         |                                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                | ,                                                                                    |                                                                                  |                                                                                              |                                                                                                  |                                                             |                                                             |                                                             |                                                               |                                           |                                                                |                                                                |                                                                              |
| ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,                                                                                                                            | ហហហហហហ                                                                                                                     | : w w w w                                                                        |                                                                         |                                                                                                                               | <br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 5555<br>511.                                                                                   | பாபாபாப                                                                              | თ თ თ თ                                                                          | ហ ហ ហ ហ<br>ម ម ម ម ម                                                                         |                                                                                                  | ა ა ა ა .<br>1.1.                                           | 5 5 5 1.<br>1.1.                                            |                                                             | <b>თ</b> თ                                                    | ין אין אי                                 |                                                                |                                                                |                                                                              |
| 5 1.8 120<br>5 1.8 121<br>5 1.8 121<br>5 1.8 122<br>5 1.8 122<br>5 1.8 122<br>5 1.8 122<br>5 1.8 122<br>5 1.8 122                                                 | 5 1.8 120<br>5 1.8 120<br>5 1.8 120<br>5 1.8 120<br>5 1.8 120<br>5 1.8 120                                                 | 5 1.8 119<br>5 1.8 119<br>5 1.8 120<br>5 1.8 120                                 | 5 1.8 118<br>5 1.8 118<br>5 1.8 119                                     | 5 1.8 116<br>5 1.8 117<br>5 1.8 117<br>5 1.8 118                                                                              | 5 1.8 116<br>5 1.8 116<br>5 1.8 116                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5 1.8 115<br>5 1.8 115<br>5 1.8 115                                                            | 5 1.8 113<br>5 1.8 113<br>5 1.8 113<br>5 1.8 114                                     | 5 1.8 112<br>5 1.8 112<br>5 1.8 112<br>5 1.8 112                                 | 5 1.8 111<br>5 1.8 111<br>5 1.8 111                                                          | 1 1 1 1 2 0 8 8 8 8                                                                              | 5 1.8<br>1.8                                                | 5 1.8                                                       | 57 57 57<br>11 12 12 12 12 12 12 12 12 12 12 12 12 1        | 5 1.8 110                                                     | 5 1.8 108<br>5 1.8 108                    | 5 1.8 108<br>5 1.8 108                                         | 5 1.8 108<br>5 1.8 108<br>5 1.8 108                            | 5 1.8 107<br>5 1.8 108<br>5 1.8 108<br>5 1.8 108                             |
| 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                             | 5 1.8 120 3 US-08<br>5 1.8 120 3 US-09<br>5 1.8 120 4 US-09<br>5 1.8 120 4 US-08<br>5 1.8 120 4 US-08<br>5 1.8 120 4 US-08 | 5 1.8 119 3 US-08<br>5 1.8 119 4 US-09<br>5 1.8 120 1 US-08<br>5 1.8 120 3 US-08 | 5 1.8 118 4 US-09 5 1.8 118 4 US-09 5 1.8 118 4 US-09 5 1.8 119 1 US-08 | 5 1.8 116 4 US-09-10/-532A-55<br>5 1.8 116 4 US-09-912-962-25<br>5 1.8 117 4 US-09-615-192A-40<br>5 1.8 118 3 US-09-085-305-2 | 5 1.8 116 2 US-08 5 1.8 116 3 US-09 5 1.8 116 4 | 5 1.8 115 4 US-09-266-965-6<br>5 1.8 115 4 US-09-107-532A-6039<br>5 1.8 115 5 PCT-US95-13658-2 | 5 1.8 113 4 US-09-<br>5 1.8 113 4 US-09-<br>5 1.8 113 4 US-09-<br>5 1.8 114 4 US-08- | 5 1.8 112 4 US-09<br>5 1.8 112 4 US-09<br>5 1.8 112 5 PCT-U<br>5 1.8 112 6 54946 | 5 1.8 111 4 US-09-252-991A-2<br>5 1.8 111 4 US-09-107-532A-5<br>5 1.8 112 1 US-07-800-364B-1 | 5 1.8 110 4 US-09-198-452A-943<br>5 1.8 110 4 US-09-464-231-15<br>5 1.8 111 4 US-09-252-991A-170 | 5 1.8 110 4 US-09<br>5 1.8 110 4 US-09<br>5 1.8 110 4 US-09 | 5 1.8 110 3 US-08<br>5 1.8 110 3 US-08<br>5 1.8 110 4 US-09 | 5 1.8 110 3 US-08<br>5 1.8 110 3 US-08<br>5 1.8 110 3 US-08 | 5 1.8 110 1 US-08-111-939-24<br>5 1.8 110 1 US-08-487-748A-15 | 5 1.8 108 4 US-09-<br>5 1.8 108 4 US-09-  | 5 1.8 108 3 US-09-<br>5 1.8 108 4 US-09-<br>5 1.8 108 4 US-09- | 5 1.8 108 2 US-07-<br>5 1.8 108 2 US-08-<br>5 1.8 108 2 US-08- | 5 1.8 107 4 US-0<br>5 1.8 108 2 US-0<br>5 1.8 108 2 US-0<br>5 1.8 108 2 US-0 |

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RESULT 2
US-09-610-185C-2
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US-09-610-185C-4
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Best Local S
Matches 32
Sequence 2, Application US/09610185C Patent No. 6573432
GENERAL INFORMATION:
APPLICANT: Borevitz, Justin
APPLICANT: Xia, Yiji
                                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 249
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09610185C Patent No. 6573432
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Borevitz, Justin
APPLICANT: Xia, Xiji
APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIGMENT
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: SALKINS.003C1
CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
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PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: (1)...(249)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                   75
                                                                                                                                         78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                   32;
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                                                                                                                                                                    Conservative
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US-09-565-538-1
US-09-561-468-1
US-09-976-145-1
US-09-976-145-1
US-09-976-155-1
US-08-480-258B-1
US-08-480-258B-1
US-08-480-258B-1
US-09-199-6378-152
US-09-328-352-4586
PCT-US96-08295-1
5466783-22
US-09-107-532A-6397
US-08-480-173A-50
US-08-480-173A-50
US-08-484-408A-50
US-08-484-408A-50
US-09-107-532A-5637
US-09-107-532A-5637
US-09-736-457-791
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                                                                                                                                                                                Score 32; DB 4; Length 249; Pred. No. 3.7e-23;
                                                                                                                                                                     Mismatches
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Sequence
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Sequence
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Sequence
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Sequence 6397, Ap
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50, Appli
54, Appl
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1, Appli
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152, App
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2, Appli
5637, Ap
791, App
791, App
791, App
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APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIC
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: SALKINS.003C1
CURRENT APPLICATION NUMBER: US/99/610,185C
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 248
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US-08-472-934-10
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Best Local
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APPLICANT: JOHNSOI
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: 06-JUN-15
CLASSIFICATION: 435
CRASCAL APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 15-May-15
PRIOR APPLICATION DATA:
                APPLICATION NUMBER: PCT/US94/0417/
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Glulio A. DeConti, Jr. Esq.
REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/354,516
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,405,941
FILING DATE: 15-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                          FILING DATE: 14-Oct-1223
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US94/11690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JOHNSON, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                            NUMBER: 08/323,460
14-Oct-1994
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METHOD AND PRODUCT FOR REGULATING
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                                                                                                                                                                                                                                                                                                                                                                                         US 08/440,421
                                                                                                PCT/US94/04178
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; Pred. No.
  CPI-004DVCP2
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; MOLECULE TYPE: protein US-08-472-934-10
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US-08-323-460A-10
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                                                                  Query Match
Best Local :
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                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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LENGTH: 1247 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELEPHONE: (617) 227-7400
                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 303/863-9700
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STREET:
DENVER
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/323,460A FILING DATE: 14-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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183 LILRLHKL 190
                          76 LILRLHKL 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOHNSON, GARY L.
ENTION: METHOD AND PRODUCT FOR REGULATING CELL
ENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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100.0%; Pr
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0; Mismatches
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Pred. No.
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o. 22;
                                                                             Length 1247;
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RESULT 5

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Query Match
Best Local Similarity
Watches 8; Conserv:
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                                                                                                             Sequence 10, Application US/08461145C Patent No. 6074861
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                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1247 amino aci
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TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
                                               NUMBER OF SEQUENCES:
                                                               APPLICANT: JOHNSON, GARY L. TITLE OF INVENTION: NOVEL M
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 21-FEB-1995
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15-APR-1993
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                                                               NOVEL MEKK PROTEINS
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Pred. No.
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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Massachusetts

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US-09-423-890-13
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Patent No. 6312934
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,145C
FILING DATE: 5-UINE-1995
CLASSIFFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 11-APR-1993
FILING DATE: 11-APR-1993
                                                         SEQ ID NO 13
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APPLICATION NUMBER: PCT/US94/11690
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04178
FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/354,516
FILING DATE: 21-FEB-1995
                                                                                                               PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/423,890 CURRENT FILING DATE: 2000-03-06
                                                                                                                                                                                                                                    APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: CPI-085CPPC
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                                                                                              NUMBER OF SEQ ID NOS
ORGANISM: Mus musculus
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NFORMATION FOR SEQ ID NO:
                                  ENGTH:
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LENGTH: 1247 amino aci
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/323,460
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TOPOLOGY: linear
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; Pred. No. 22
0; Mismatches
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                                                   ; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosofophila
US-09-058-489-4
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                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09058489 Patent No. 6103886 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
                                                                                                                        SEQ ID NO 4
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Query Match
Best Local Similarity
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                                                                                                                                    EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
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APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No.
TITLE OF INVENTION: the Y Chromosome
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                                                                                                                                                                                                                                                FILE REFERENCE: WHI97-08pA
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                                                                                                                                                                                                                                                                                                                                      APPLICANT: Whitehead Institute for Biomedical Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SARLIER APPLICATION NUMBER: 08/440,421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: Johnson, Gary L.
ITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARLIER FILING DATE: 1995-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 LILRLHKL 540
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100.0%;
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 Score 7; DB 3; Pred. No. 18;
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Pred. No.
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US-08-722-626B-2
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US-09-252-991A-26955
                                                     RESULT 12
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SEQ ID NO 26955
LENGTH: 218
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SEQ ID NO 20768
LENGTH: 183
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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1998-02-18
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; ORGANISM: Acinetobacter baumannii US-09-328-352-6229
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                             GENERAL INFORMATION:
APPLICANT: GATY L. BIFETON et al.
APPLICANT: GATY L. BUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6229
LENGTH: 289
TYPE: PRT
                                                                                                                                                                                                                                Sequence 6229, Application US/09328352 Patent No. 6562958
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Best Local Similarity
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Pat Hagan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                          51 KSCRLRW 57
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Pred. No.
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TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-000110US
CURRENT APPLICATION NUMBER: US/09/495,406
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
NUMBER: OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 301
TYPE: PRT
TORGANISM: Campylobacter jejuni
US-09-495-406-15
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Best Local Similarity
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US-08-671-320-11
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APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09495406 Patent No. 6503744
APPLICATION NUMBER: US/08/671,320
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VIERLII
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VIERLING JR, RICHARD A
TITLE OF INVENTION: A SOVBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO. 103RD STREET
                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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nes 7; Conservative (
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ZIP: 68124-1076
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100.0%; Pred. No. 65;
ive 0; Mismatches
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| Sequence 17572, A Sequence 401, App Sequence 1191, App Sequence 3167, Ap Sequence 16266, A Sequence 16266, A Sequence 161, App Sequence 14, Appl Sequence 15522, A Sequence 22, Appl Sequence 23, Appl Sequence 21516, App                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Sequence 100, App<br>Sequence 156, App<br>Sequence 3534, App<br>Sequence 1567, App<br>Sequence 126, App<br>Sequence 4876, App<br>Sequence 7686, Ap                                                                                                                                                                                               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                                                                                                          | Sequence 1100, Ap<br>Sequence 9193 Ap<br>Sequence 9462, Ap<br>Sequence 1646 Ap<br>Sequence 1314, Ap<br>Sequence 4876 Ap<br>Sequence 5004, Ap<br>Sequence 393, App                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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Ap Sequence 30971, A Sequence 50, Appl Sequence 45991, A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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| -10-124-821<br>-10-124-823<br>-10-125-932<br>-10-125-932<br>-10-152-395<br>-10-152-395<br>-10-152-396<br>-10-153-552<br>-10-153-840                   | -10-121-052<br>-10-121-053<br>-10-121-063<br>-10-121-063<br>-10-123-212<br>-10-123-213<br>-10-123-221<br>-10-123-771<br>-10-123-911          | 10-152-377<br>-10-152-377<br>-10-152-386<br>-10-152-399<br>-10-152-399<br>-10-152-399<br>-10-157-785<br>-10-157-794<br>-10-157-794<br>-10-157-796<br>-10-160-500<br>-10-160-500 | -10 124 -816 -10 -124 -820 -10 -124 -820 -10 -125 -927 -10 -125 -927 -10 -125 -925 -10 -125 -825 -10 -125 -825 -10 -125 -825 -10 -125 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -145 -825 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -275 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -155 -10 -15 | US-10-139-980-4 US-10-142-762-4 US-10-142-766-4 US-10-145-625-4 US-10-145-920-4 US-10-145-960-4 US-10-147-98-4 US-10-147-98-4 US-10-147-516-4 US-10-147-516-4 US-10-147-516-4 US-10-147-516-4 US-10-147-516-4 US-10-147-516-4 US-10-123-050-4 US-10-123-050-4 US-10-121-059-4 US-10-123-109-4 US-10-123-109-4 US-10-123-109-4 US-10-123-109-4 US-10-123-157-4 US-10-123-157-4 US-10-123-157-4 US-10-123-157-4 |
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| <b>ຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓ</b>                                                                                                                                                                                                | , o,                                                                                                                                                                                                                                                                                                                                                                 | n o o o o o o o o o o o o o o o o o o o                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | . თ თ თ თ თ თ თ თ თ                                                                                                                    |
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| -10-128-6927A<br>-10-140-927A<br>-10-10-13-392-2<br>-10-066-500-4<br>-10-058-072-4<br>-10-028-072-4<br>-10-121-049-4<br>-10-123-904-4<br>-10-123-904-4<br>-10-175-746-4<br>-10-176-918-4<br>-10-176-918-4<br>-10-002-796-4<br>-10-002-796-4 | -10-147-537-88<br>-10-152-381-894<br>-10-152-381-894<br>-10-152-400-4894<br>-10-153-585-4894<br>-10-157-780-4894<br>-10-157-780-4894<br>-10-157-801-4894<br>-10-157-801-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894<br>-10-158-789-4894 | US-10-140-809-484 US-10-140-810-484 US-10-140-810-484 US-10-141-865-484 US-10-141-703-484 US-10-141-703-484 US-10-141-706-484 US-10-141-757-484 US-10-141-762-484 US-10-141-762-484 US-10-142-428-484 US-10-142-428-484 US-10-142-428-484 US-10-142-430-484 US-10-142-484-484 US-10-143-113-484 US-10-143-13-484 US-10-145-871-484 US-10-145-871-484 US-10-145-871-484 US-10-145-871-484 US-10-145-871-484 US-10-145-871-484 US-10-145-871-484 US-10-145-871-484 US-10-146-792-484 US-10-146-792-484 US-10-146-793-484 US-10-146-793-484 US-10-146-793-484 US-10-147-507-484 US-10-146-793-484 US-10-146-793-484 US-10-146-793-484 US-10-146-793-484 US-10-146-793-484 US-10-146-793-484 US-10-147-507-484 | -10-156-842-48 -10-156-844-48 -10-156-845-48 -10-156-846-48 -10-123-913-48 -10-123-923-48 -10-140-020-48 -10-140-020-48 -10-140-030-48 |
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| ហេសហហេសហហេសហហេស                                                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 63311111111                                                                                                                            |
| 5 US-10                                                                                                                                             | US-10<br>US-10<br>US-10<br>US-10<br>US-10<br>US-10<br>US-10<br>US-10<br>US-10<br>US-10<br>US-10                                                                                                                                                                                                                                                                                                          | 5 US-10-12-42-32-3-5 US-10-12-10-12-05-0 US-10-12-10-12-05-0 US-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-10-12-12-12-12-12-12-12-12-12-12-12-12-12-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 63 15 US-10                |

| 741<br>742<br>743<br>744                                                                              | 739<br>740                                                  | 737<br>738                             | 735<br>736                             | 733                                    | 731               | 729                                    | 727<br>728                             | 725<br>726                         | 724               | 722<br>723                             | 721                                | 719               | 717                     | 715<br>716                              | 713               | 712               | 710                                    | 708<br>709                             | 706<br>707                             | 704<br>705                         | 703              | 701                                  | 699              | 697                                   | 696<br>695                          | 694                 | 692              | 690<br>691                              | 689               | 687              | 686<br>686<br>5                    | 684                 | 682<br>683                           | 681             | 679<br>680                         | 678              | 676                                | 675            |
|-------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|----------------------------------------|----------------------------------------|----------------------------------------|-------------------|----------------------------------------|----------------------------------------|------------------------------------|-------------------|----------------------------------------|------------------------------------|-------------------|-------------------------|-----------------------------------------|-------------------|-------------------|----------------------------------------|----------------------------------------|----------------------------------------|------------------------------------|------------------|--------------------------------------|------------------|---------------------------------------|-------------------------------------|---------------------|------------------|-----------------------------------------|-------------------|------------------|------------------------------------|---------------------|--------------------------------------|-----------------|------------------------------------|------------------|------------------------------------|----------------|
| n თ თ თ თ                                                                                             | , o, o,                                                     | თთ                                     | თთ                                     | <i>y</i> ov o                          | י סי              | <b>0</b> 0                             | თთ                                     | თთ                                 | , ON (            | י טיע                                  | თ თ                                | . თ ი             | ب ص                     | a o                                     | თ თ               | 000               | י טי                                   | თთ                                     | თ თ                                    | თ თ                                | თი               | n on o                               | n 00 (           | n on                                  | თ თ                                 | ი თ                 | , o              | <b>D</b> O                              | თი                | ח סח             | σ σ                                | · σ ·               | თთ                                   | , 00 (          | <b>თ</b> თ                         | თ                | ש פי                               | თ თ            |
|                                                                                                       |                                                             |                                        |                                        |                                        |                   |                                        |                                        |                                    |                   |                                        |                                    |                   |                         |                                         |                   |                   |                                        |                                        |                                        |                                    |                  |                                      |                  |                                       |                                     |                     |                  |                                         |                   | •                |                                    |                     |                                      |                 |                                    |                  | •                                  |                |
| 2263<br>263<br>363                                                                                    | 263<br>263                                                  | 263<br>263                             | 263<br>263                             | 263                                    | 263               | 263<br>263                             | 263<br>263                             | 263<br>263                         | 263               | 263                                    | 263                                | 263               | 263                     | 263<br>263                              | 263               | 263               | 263                                    | 263<br>263                             | 263<br>263                             | 263<br>263                         | 263              | 263                                  | 263              | 263                                   | 263<br>263                          | 263                 | 263              | 263<br>263                              | 263               | 263              | 263                                | 263                 | 263<br>263                           | 263             | 263                                | 263              | 263                                | 263            |
| 155                                                                                                   | 555                                                         | 15<br>15                               | 15                                     | 15                                     | 15                | 15<br>15                               | 15<br>15                               | 15                                 | 15                | 15                                     | 15                                 | 15                | 15                      | 15                                      | 15                | 15                | 15                                     | 15                                     | 15<br>15                               | 15                                 | 15               | 155                                  | 15               | 7 15                                  | 15<br>15                            | 15                  | 15               | 15                                      | 15                | 15               | 15                                 | 15                  | 15<br>15                             | 15              | 15                                 | 15               | 1<br>7<br>5                        | 15             |
| US-10-223-084-182<br>US-10-223-098-182<br>US-10-223-098-182<br>US-10-223-087-182<br>US-10-223-087-182 | -10-194-359-4E<br>-10-226-739-41                            | -10-223-085-18<br>-10-192-007-48       | -10-121-042-48<br>-10-123-912-48       | -10-158-785-48<br>-10-158-785-48       | -10-137-869A-48   | -10-131-835A-4<br>-10-137-864A-4       | -10-131-822A-48<br>-10-131-828A-48     | -10-131-817A-48<br>-10-131-821A-48 | -10-131-815A-48   | -10-131-825A-48<br>-10-230-417-484     | -10-128-694A-48<br>-10-128-694A-48 | -10-128-688A-48   | -10-127-844A-4          | -10-127-836A-48<br>-10-127-841A-48      | -10-127-834A-48   | -10-127-832A-48   | -10-127-828A-48                        | -10-127-826A-48<br>-10-127-827A-48     | -10-127-822A-48<br>-10-127-824A-48     | -10-125-928A-48<br>-10-127-821A-48 | -10-125-921A-484 | -10-123-907-48                       | -10-158-78       | -10-137-868-48<br>-10-147-492-48      | -10-123-235-48<br>-10-124-818-48    | -10-121-051-48      | -10-121-040-48   | -10-147-512-48<br>-10-175-735-48        | -10-147-508-48    | -10-146-791-48   | -10-131-836A-48<br>-10-146-729-484 | -10-131-829A-48     | -10-128-691A-484<br>-10-131-819A-484 | -10-128-690A-48 | -10-128-684A-48<br>-10-128-686A-48 | -10-127-851A-48  | -10-127-849A-48<br>-10-127-850A-48 | -10-1          |
| quenc<br>quenc<br>quenc                                                                               | equence 484, equence 41,                                    | equence 182, equence 484,              | equence 484,<br>equence 484,           | equence 484,                           | equence 484       | equence 484,                           | equence 484, equence 484,              | equence 484,<br>equence 484,       | equence 484,      | equence 484,                           | equence 484,<br>equence 484,       | equence 484,      | equence 484,            | equence 484,<br>equence 484,            | equence 484,      | equence 484,      | equence 484,                           | equence 484,<br>equence 484,           | equence 484,<br>equence 484,           | equence 484,<br>equence 484,       | equence 484,     | equence 484,                         | equence 484,     | equence 484,                          | equence 484,<br>equence 484,        | equence 484,        | equence 484,     | equence 484,<br>equence 484.            | equence 484,      | equence 484,     | equence 484,<br>equence 484,       | equence 484,        | equence 484,<br>equence 484,         | equence 484,    | equence 484,<br>equence 484.       | equence 484,     | equence 484,                       | equence 484,   |
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| 814<br>815<br>816<br>817                                                                              | 812<br>813                                                  | 810<br>811                             | 808                                    | 806                                    | 408               | 802<br>803                             | 800<br>801                             | 798<br>799                         | 797               | 795<br>796                             | 794                                | 792               | 790                     | 788<br>789                              | 787               | 785               | 783<br>784                             | 781<br>782                             | 779<br>780                             | 778                                | 776              | 774                                  | 772              | 770<br>771                            | 768<br>769                          | 767                 | 765              | 763<br>764                              | 762               | 760<br>761       | 759<br>759                         | 757                 | 755<br>756                           | 754             | 753                                | 751              | 749<br>750                         | 748            |
| <b>ი ი ი ი</b>                                                                                        | , 0, 0                                                      | 00                                     | 0 00                                   | <b>ታ</b> ወ ር                           | ע ע               | თთ                                     | თთ                                     | σ, σ                               | , 0, 0            | שש                                     | თ თ                                | , 00 (            | יסע                     | ത ത                                     | თσ                | 000               | ש ע                                    | თ თ                                    | თ თ                                    | თ თ                                | <b>σ</b> σ       | n 01 (                               | ח מ              | <b>D</b> D                            | თ თ                                 | თ ი                 | n 01             | თ თ                                     | o 0               | ע ע              | თ თ                                | n 01                | თ თ                                  | 100             | თ თ                                | , o o            | ש מ                                | თი             |
| 00000                                                                                                 |                                                             |                                        |                                        |                                        |                   |                                        |                                        |                                    |                   |                                        |                                    |                   |                         |                                         |                   |                   |                                        |                                        |                                        |                                    |                  |                                      | •                |                                       |                                     |                     | •                |                                         |                   | •                |                                    | •                   |                                      |                 |                                    |                  |                                    |                |
|                                                                                                       | 313                                                         | 313                                    | 313                                    | 313                                    | 313               | 313<br>313                             | 313                                    | 313                                | 313               | 313                                    | 313                                | 313               | 2 2 1<br>2 2 1<br>3 2 1 | 313<br>313                              | 313               | 313               | 313                                    | 313<br>313                             | 313                                    | 313                                | 313              | 313                                  | 308              | 305                                   | 294<br>305                          | 290                 | 287              | 284<br>285                              | 284               | 277              | 276                                | 274                 | 271                                  | 263             | 263                                | 263              | 263                                | 263            |
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| 1 US-09-997-683-414<br>1 US-09-997-683-414<br>1 US-09-989-729A-414<br>1 US-09-997-349-414             | US-09-990-443-414<br>US-09-991-854-414<br>US-09-997-639-414 | US-09-997-559-414<br>US-09-997-601-414 | US-09-991-172-414<br>US-09-990-726-414 | US-09-997-514-414<br>US-09-997-573-414 | US-09-990-437-414 | US-09-989-726-414<br>US-09-998-156-414 | US-09-990-562-414<br>US-09-990-711-414 | US-09-990-438-414                  | US-09-997-428-414 | US-09-997-653-414<br>US-09-993-667-414 | US-09-989-734-414                  | US-09-990-436-414 | US-09-991-181-414       | US-09-990-444-414<br>US-09-738-626-3724 | US-09-989-735-414 | US-09-992-598-414 | US-09-990-456-414<br>US-09-989-721-414 | US-09-991-163-414<br>US-09-993-604-414 | JS-09-991-073-414<br>JS-09-990-442-414 | JS-09-989-732-414                  | S-09-989-727-414 | S-09-989-723-414<br>S-09-989-723-414 | US-10-306-762-22 | US-10-317-832-106<br>US-10-138-098-50 | 3-09-826-508-4<br>JS-10-317-832-105 | JS-10-369-493-13439 | JS-10-081-816-22 | JS-10-370-685-132<br>JS-10-156-761-9562 | US-10-080-608A-43 | US-10-253-007-34 | US-10-254-049-2792                 | JS-10-369-493-13320 | 5-10-369-493-22102                   | -10-153-934-484 | -10-146-788-484<br>-10-152-380-484 | 3-10-146-727-484 | -10-137-866-484<br>-10-146-726-484 | 10-223-089-182 |

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| -10-173-703                                                                                                                                                                                              | -10-176-754-<br>-10-176-759-<br>-10-176-920-<br>-10-176-920-<br>-10-176-922-<br>-10-176-984-<br>-10-179-508-<br>-10-179-512-<br>-10-179-512-<br>-10-179-512-<br>-10-179-512-<br>-10-179-512-<br>-10-179-512- | -10-174-569<br>-10-174-583-<br>-10-174-589-<br>-10-174-589-<br>-10-175-736-<br>-10-175-736-<br>-10-175-744-<br>-10-175-745-<br>-10-175-745-<br>-10-175-745-<br>-10-175-751-<br>-10-175-751-<br>-10-176-489-                                                                                                                                                                                                                                                                                                                                                                                                  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FILE REFERENCE: EP01-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 274
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                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-10-033-190-2
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                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10033190
Publication No. US20020133848A1
GENERAL INFORMATION:
APPLICANT: Excitais Plant Sciences,
TITLE OF INVENTION: IDENTIFICATION /
TITLE OF INVENTION: TOMATO
                                                                                                    Query Match
Best Local Similarity
Matches 274; Conserv
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                                                MNSTSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYL
               RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKI
RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKI
                                                                                                    100.0%; ilarity 100.0%; Conservative 0
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US-10-063-705-89
US-10-063-710-88
US-10-063-711-88
US-10-063-711-88
US-10-063-713-88
US-10-063-713-88
US-10-063-715-88
US-10-063-712-88
US-10-063-721-88
US-10-063-731-88
US-10-063-731-88
US-10-063-731-88
US-10-063-731-88
US-10-063-731-88
US-10-063-731-88
US-10-063-744-88
US-10-063-578-88
                                                                                                       0;
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Pred. No. 3.8e-265;
Mismatches 0;
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                                                                                                                              Length 274;
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APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT APPLICATION NUMBER: 60/227439
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-08-2
PRIOR PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOSTWARE: Patentin version 3.1
SEQ ID NO 480
LENGTH: 209
TYDEN: DET
                                                                                                                                            US-09-934-455-482; Sequence 482, Application No.
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US-09-934-455-480
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Publication No. US:
GENERAL INFORMATIO
APPLICANT: Adam,
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Best Local S
Matches 32
                                                                                                                                 GENERAL INFORMATION
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APPLICANT:
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APPLICANT:
            APPLICANT:
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                                                                                                                                                                                                                                          78 LRIHKLIGNRWSLIAGRIPGRTANDVKNYWNT 109
                                                                                                                                                                                                                           75 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
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         Creelman, Robert
Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
Reuber, Lynne
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Riechmann, Jose Luis
Yu, Guo-Liang
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Dubell, Arnold
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Jiang, Cai-Zhong
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Ratcliffe, Oliver
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                                                                                                                                                          Application US/09934455
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llarity 100.0%;
Conservative
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1.2e-23;
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Guo-Liang

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; ORGANISM: Arabidopsis thaliana
US-09-934-455-14
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CURRENT APPLICATION NUMBER: US/09/934,455

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/227439

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: MBI-0022

PRIOR APPLICATION NUMBER: MBI-0023

PRIOR APPLICATION NUMBER: MBI-0023

PRIOR APPLICATION NUMBER: MBI-0023

PRIOR APPLICATION NUMBER: MBI-0023

PRIOR FILING DATE: 2001-04-17
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 249
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 482
                                                                          Matches
                                                                                              Query Match
Best Local :
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Publication No
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT ETLING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ILE REFERENCE: MBI-0025
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TTLE OF INVENTION: Genes for Modifying Plant Traits
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ITLE OF INVENTION: Genes for Modifying Plant Traits
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75 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                          78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
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                                                                                              Similarity
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Heard, Jacqueline
Jiang, Cai-Zhong
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; Pred. No. 1.4e-23;
                                                                                            Score 32;
Pred. No.
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                                                                            Mismatches
                                                                                              1.4e-23;
                                                                                                              Length 249
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SOFTWARE: PatentIn Ver.
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              Sequence 438, Application US/09934455 Publication No. US20030121070A1
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                                                                                                           APPLICANT:
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CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT EILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
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                                                                     APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
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PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-10-06
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 249
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APPLICATION NUMBER: 60/113,409
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Jiang, Cai-Zhong
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Pilgrim, Marsha
Ratcliffe, Oliver
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Dubell, Arnold
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Zhang, James
Benito, Maria-Ines
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Reuber, Lynne
Jiang, Cai-Zhong
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Riechmann, Jose Luis
Yu, Guo-Liang
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Adam, Luc
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PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 438
LENGTH: 212
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-443-704-6
SEQ ID NO 6
LENGTH: 120
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/443,704
CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: 60/109,294
EARLIER FILING DATE: NO. US20020066120Alember 20,
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shi, June
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
FILE REFERENCE: BB1280 US NA
                                                                          PRIOR APPLICATION NUMBER: 60/109,294
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
                                                                                                                                   APPLICANT: Cahoon, Rebecca E.
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 USDIV
CURRENT APPLICATION NUMBER: US/10/008,118A
CURRENT FILING DATE: 2001-12-05
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APPLICANT: Rafalski, Antoni
                                                             SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 120
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Pred. No. 1.2e-1
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Pred. No.
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hes 0;
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US-10-407-920-29
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SOFTWARE: Patentin version 3.1
SEQ ID NO 390
LENGTH: 203
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Best Local
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 203
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APPLICANT: Adam, Lu
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                                                                 APPLICANT: Shi, Lifang TITLE OF INVENTION: MYB Transcription Factors FILE REFERENCE: 38-21(52703)A CURRENT APPLICATION NUMBER: US/10/407,920 CURRENT FILLING DATE: 2003-66-06 PRIOR APPLICATION NUMBER: US/60/370,759 PRIOR FILLING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT PILING DATE: 2001-08-22
ERIOR APPLICATION NUMBER: 60/22/439
ERIOR FILING DATE: 2000-08-22
ERIOR APPLICATION NUMBER: MBI-0022
ERIOR FILING DATE: 2001-11-16
ERIOR FILING DATE: 2001-11-16
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TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
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Ratcliffe, Oliver
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Jiang, Cai-Zhong
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100.0%; Pred. No.
tive 0; Mismatc
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1.1e-05;
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Sequence 22, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT APPLICATION NUMBER: 05/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63
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US-10-021-811-22
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PRIOR ETLING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-417
NUMBER OF SEQ ID NOS: 516
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SEQ ID NO 70
LENGTH: 219
TYPE: PRT
ORGANISM: Arabidopsis thaliana
S-09-934-455-70
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CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
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   SOFTWARE: Microsoft Office 97
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Pilgrim, Marsha
Ratcliffe, Oliver
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Jiang, Cai-Zhong
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100.0%; Pred. No. 1.2e-05;
ative 0; Mismatches 0;
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100.0%; Pred. No.
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PEATURE:
NAME/KEY: UNS.
LOCATION: (53)
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            GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
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CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
                                                                                                                                                                     Sequence 60, Application US/100 Publication No. US20030024007A1
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LENGTH: 115
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Best Local Similarity
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APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
PRIOR APPLICATION NUMBER: 60/110,609
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NAME/KEY: UNSURE
LOCATION: (113)..(114)
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                                                                                                                                                                                                                                                                                 61 KSCRLRWLNYLRP 73
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100.0%; Pred. No.
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Pred. No. 6.8e-05
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Gaps

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Sequence 18, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:

APPLICANT: Caboon, Rebecca E.

APPLICANT: Caboon, Rebecca E.

APPLICANT: Weng, Yiwen

APPLICANT: Weng, Yiwen

APPLICANT: Weng, Zude

TITLE OF INVENTION: Plant Myb Transcription Factor Homologs

FILE REFERENCE: BB1294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/110,609

PRIOR APPLICATION NUMBER: 60/110,609

PRIOR FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOPTWARE: Microsoft Office 97

SEQ ID NO 18

LENGTH: 145

TYPE: PRT

ORGANISM: Oryza sativa
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NUMBER OF SEQ ID NOS: 63
SOPTWARE: Microsoft Office 97
SEQ ID NO 60
LENGTH: 131
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: UNSURE
LOCATION: (127)
NAME/KEY: UNSURE
LOCATION: (111)
NAME/KEY: UNSURE
LOCATION: (112)
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Search completed: January 29, 2004, 20:26:32 Job time : 47 secs
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| Mailori                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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| Catanalation   Cata   | 420<br>420<br>420                                                                                     | 418<br>418                                               | 412<br>413                                               | 410                                  | 402<br>403                           | 399<br>402                           | .397<br>398                          | 395<br>396                           | 394<br>394                           | 394                | 2 0 0<br>0 0<br>0 0                  | <br>9 0 1<br>0 0 1                   | 392                                  | 388<br>886                                                                      | 388                                   | 387                                  | 387                                                | 386                                  | 384                                  | 380<br>383                           | 378<br>378                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 377<br>378                           | 375                                  | 373                                  | 372                  | 372              | 371                                  | 370<br>371                           | 370                                       | 365<br>265                           | 365              | 363                 | 362                                  | 361              | 359              | 358              |
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Ф                           | <br>≱.e                              | ni<br>ni                             | 0 1                                  | te<br>e                              | i de d             | 7 B.7                                | י טי כ                               | , E F                                | ה ל<br>ה                                                                        | 22                                    |                                      | היה לי                                             | # K                                  | lo                                   | t t                                  | po<br>o s                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | d t<br>e                             | C. 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| apolipoprotein apolipoprotein hypothetical proporteical p | 2.2 471<br>2.2 471<br>2.2 471<br>2.2 471<br>2.3 471<br>2.4 473<br>2.3 473<br>2.3 473                  | 2.2 467 2                                                | 2.2 466 1<br>2.2 466 2                                   | 2.2 464 2<br>2.2 464 2               | 2.2 462 2<br>2.2 462 2               | 2.2 462 2<br>2.2 462 2               | 2.2 462 1<br>2.2 462 2               | 2.2 461 2<br>2.2 461 2               | 2.2 461 2                            | 2.2 459 2          | 2.2 458 2                            | 2.2 458 2                            | 2.2 456 2                            | 2.2 456 2                                                                       | 2.2 452 2                             | 2.2 452 1                            | 2.2 450 2                                          | 2.2 450 2                            | 2.2 447 2                            | 2.2 446 2<br>2.2 446 2               | 2.2 445 2<br>2.2 446 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 2.2 443 2<br>2.2 443 2               | 2.2 442 2                            | 2.2 441 2                            | 2.2 440 2            | 2.2 439 2        | 2.2 439 2                            | 2.2 437 1<br>2.2 439 1               | 2.2 434 2                                 | 2.2 433 2                            | 2.2 432 2        | 2.2 431 2           | 2.2 428 2                            | 2.2 426 2        | .2 425 2         | 2.2 422 2        |
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| <b>ຑຑຑຑຑຑຑຑ</b> ຑ                                                                                                                                                                            |                                                                                                                                                                                                   | <b>๑๑๑๑๑๑๑๑๑</b> ๑                                                                                                                                                                                                                                    | , o,                                                                                                                                                                                                                                                                                                                                                                        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| hypothetical prote polypeptide N-acet glutathionylspermi peptidyl-prolyl ci probable TNP2-like PTS system, fructo phosphinothricin-t glutamate synthase segment polarity p DNA topoisomerase | hyp<br>ATP<br>inn<br>GTP<br>hyp<br>pro<br>hyp                                                                                                                                                     | single-stranded-dn hypothetical prote hypothetical prote two-component sens probable pectinest hypothetical prote hypothetical prote hypothetical prote pectinesterase (EC probable pectinest                                                         | cytochrome P450 en acetolactate synth acetolactate synth phosphomannomutase cyclophilin C-asso DNA modification m ABC transporter AT hypothetical prote neopullulanase (EC hypothetical prote protection of the pr | hypothetical prote ampG protein, prob ampG protein, prob gene gli protein - glutathione-disulf hypothetical prote acctolactate synth hypothetical prote pTS system, lactos phosphotransferase hypothetical grote hypothetical f 2.8K                                     | hypothetical prote thermosome beta ch probable ABC trans polyketide synthas polyketide synthas hypothetical prote cytochrome-c oxida paraquat-inducible protein-tyrosine-p xylosidase/arabino SH2-domain protein cytochrome-c oxida arginyl-tRNA synth calcium-dependent probable cytochrom hypothetical prote propanediol dehydr propanediol dehydr unknown protein, 7 probable membrane K+-transporting AT long-chain-fatty-a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

| 901<br>902<br>904                                                                   | 898<br>868                                                    | 896<br>897                       | 894<br>895     | 892                | 890<br>108     | 889<br>888                      | 887           | 885<br>886                               | 884            | 882<br>883                       | 881            | 880                | 878            | 877            | 875               | 874            | 872<br>873     | 871            | 869<br>870     | 868            | 866            | 8 6<br>4 7<br>4 7 | 863            | 861                | 859<br>860     | 858              | 856            | 00 00<br>U U<br>14 (U | 853            | 85<br>5<br>7   | 850            | 849            | 847           | 846           | 9 4 4<br>7 4   | 843                | 842               | 840            | 839                | 838            | 836                | 00 u               |
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| തെതത                                                                                | አወወ                                                           | o o                              | <b>თ</b> თ (   | n on (             | ע ע            | თთ                              | 101           | თ თ                                      | , O +          | თ თ                              | , o,           | თ თ                | n 01           | o o            | n 01              | <b>o</b> (     | ח מי           | 6              | ກຸດາ           | თი             | n 01 (         | ን ዕነ              | ο ο            | י טי               | თთ             | თ თ              | , O) (         | თ თ                   | 0              | יס ת           | , o            | თ ი            | n on          | on 0          | ח סי           | , o                | თ ი               | n o            | 6 (                | თσ             | , 0,               | თ თ                |
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| 766<br>766<br>767<br>768                                                            |                                                               |                                  |                |                    |                |                                 |               |                                          |                |                                  |                |                    |                |                |                   |                |                |                |                | •              |                |                   |                |                    |                |                  |                |                       |                |                |                |                |               |               |                |                    |                   |                |                    |                |                    |                    |
| 2 AC0985<br>2 A40258<br>2 B84594<br>2 JC6564                                        |                                                               |                                  |                |                    |                |                                 |               |                                          |                |                                  |                |                    |                |                |                   |                |                |                |                |                |                |                   |                |                    |                |                  |                |                       |                |                |                |                |               |               |                |                    |                   |                |                    |                |                    |                    |
| 5555555<br>5644<br>644                                                              | 149                                                           | 423<br>750                       | 575            | 250                | TUGB<br>878    | 015                             | 544           | 876<br>128                               | 769            | 1923<br>115K                     | 635            | 798                | 026            | 001            | 130               | 575            | #20<br>#420    | 900            | 660<br>827     | 533            | 283            | 784<br>467        | 429            | 251                | 276            | 268              | 452            | 218                   | 319            | 432            | 013            | FMA            | 999           | 129           | 575            | 895                | 587               | 331            | 046                | 163            | 810                | 602                |
|                                                                                     |                                                               |                                  |                |                    |                |                                 |               |                                          |                |                                  |                |                    |                |                |                   |                |                |                |                |                |                |                   |                |                    |                |                  |                |                       |                |                |                |                |               |               |                |                    |                   |                |                    |                |                    |                    |
| probable polysacch RAS GTPase-activat probable LRR recep cellobiose oxidase         | trans<br>hypot                                                | trans<br>proba                   | C-eki          | compl              | gluce          | primo                           | photo         | ZC21.<br>P3A2                            | hypot          | trans                            | hypot          | isoud<br>Isoud     | Isoud          | isoud<br>Jeond | phosp             | C-8ki          | conse          | trans          | histi          | hypot          | hypot          | phyco             | hypot          | hypot              | aceta          | epide            | hypot          | henat                 | hypot          | amino          | hypot          | trans          | DNA 1         | DNA 1         | C-ski          | hypot              | proba             | ATP-d          | seler              | hypot          | sna41              | hypoth             |
| probable LRR re probable LRR re cellobiose oxic                                     | sformin<br>hetica                                             | sformin<br>able AT               | prote          | lex I i            | cortic         | c 82 k                          | system        | ZC21.4 protein - C<br>P3A2 DNA binding p | hetica         | sformin<br>sformin               | hetica         | onocran<br>ohate a | hotran         | ohate a        | hate a            | prote          | erved h        | lation         | dine r         | hetica         | hetica         | biliso            | hetica         | hetica             | hetica         | ermal a          | hetica         | Checica               | hetica         | acid           | hetica         | .Hecrea        | igase         | igase,        | prote          | hypothetical p     | ible WD           | P-dependent h  | ocyste             | hetica         | sna41 protei       | nismacci<br>hetica |
| lysacch<br>lysacch<br>activat<br>R recep<br>oxidase                                 | g prot                                                        | g prot                           | in FB2         | nterme             | oid re         | Da pro<br>protei                | I pro         | ein - :                                  | 1 prot         | o prot                           | 1 prot         | sacety<br>cetylt   | sacety         | cetylt         | cetylt            | in FB2         | ypothe         | initi          | ich ca         | l prot         | 1 prot         | me anci           | l prot         | l prot             | ligas          | sease<br>utoant  | 1 prot         | nuclea<br>I prot      | l prot         | transp         | 1 prot         | d brot         | (NAD)         | NAD-de        | FB2            | prot               | 40 1              | į ir           | ne-s               | 1 prote        | р,<br>П            | prot               |
| 0.01151                                                                             | <i>y</i> ( <i>y</i> ( <i>y</i>                                | יטו כן                           |                | , 125 (1           | , ,,           | ٠. ح                            | ,,,           | J (1                                     |                |                                  | ν.             | ', -               | -,-            | • • • •        | , ',              | ω.             |                | ,              |                |                |                | <b>,</b>          |                |                    |                | ٠.,              |                | , 10                  | ι,             |                |                |                | , –           |               | , ,            |                    | •                 | •              |                    |                |                    |                    |
|                                                                                     |                                                               |                                  |                |                    |                |                                 |               |                                          |                |                                  |                |                    |                |                |                   |                |                |                |                |                |                |                   |                |                    |                |                  |                |                       |                |                |                |                |               |               |                |                    |                   |                |                    |                |                    |                    |
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| 974<br>974<br>975<br>976                                                            | 971<br>972<br>973                                             | 969<br>970                       | 967<br>968     | 0 6 6 6            | 963            | 961<br>962                      | 960           | 959<br>826                               | 957            | 956<br>955                       | 954            | 953                | 951            | 950            | 948               | 947            | 945<br>946     | 944            | 942<br>943     | 941            | 939            | 937               | 936            | 934                | 932            | 931              | 929            | 928                   | 926            | 924            | 923            | 922            | 920           | 919           | 917            | 916                | 915               | 913            | 912                | 911<br>911     | 909                | 908                |
| <b>aaaa</b> a                                                                       | ש ט ט                                                         | თ თ                              | തത             | νοι                | ח ע            | თთ                              | , D, (        | <b>თ</b> თ                               | ο ,            | თთ                               | , o            | თ თ                | n 01           | თ თ            | n 01              | 6 6            | <b>a</b> o     | σ,             | ש ש            | ი ი            | , o, (         | ש פע              | σ σ            | , 0, (             | س ص            | თ თ              | . 6            | ח ס                   | , O (          | ח ס            | , o            | თ თ            | n 01          | σ, ο          | n on           | . 0                | თ ი               | n 01           | σ.                 | თ თ            | <b>,</b> 0,        | თ თ                |
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| 963<br>958<br>958<br>958                                                            | 940<br>940<br>640                                             | 932<br>933                       | 929<br>930     | 924                | 923            | 920<br>922                      | 908           | 907<br>908                               | 902            | 900<br>902                       | 895            | 894                | 894            | 894            | 892               | 892            | 890            | 890            | 886            | 986            | 8 5            | 8.81<br>8.83      | 878            | 874                | 859<br>859     | 857              | 837            | 837                   | 832            | 819            | 810            | 809            | 805           | 805           | 804            | 804                | 804               | 798            | 7.90               | 785            | 777                | 775                |
| 2 S62<br>2 A70<br>2 T26                                                             |                                                               |                                  |                |                    |                |                                 |               |                                          |                |                                  |                |                    |                |                |                   |                |                |                |                |                |                |                   |                |                    |                |                  |                |                       |                |                |                |                |               |               |                |                    |                   |                |                    |                |                    | 2 F860:            |
| S62065<br>A70634<br>A70634<br>S54461<br>T26022                                      | 120<br>120                                                    | 4D<br>161                        | 923            | 926                | 3 p G          | 066                             | 327           | 352<br>722                               | 587            | 351<br>079                       | 640            | 372                | 719            | 221            | 3661              | 985            | 991            | 654            | 825            | 625            | 310            | 026               | 767            | 398                | 242            | 883              | 777            | 572                   | 230            | 744            | 696            | 312            | 717           | 719           | 208            | HSI                | CIB               | 022            | 542                | 180            | IUGA               | 026                |
|                                                                                     |                                                               |                                  |                |                    |                |                                 |               |                                          |                |                                  |                |                    |                |                |                   |                |                |                |                |                |                |                   |                |                    |                |                  |                |                       |                |                |                |                |               |               |                |                    |                   |                |                    |                |                    |                    |
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| alanie<br>alanie<br>probable<br>hypothet<br>hypothet                                | alyi tRN<br>valine-t<br>nrohahla                              | penicill<br>progeste             | rep-1 proceste | hypothet           | progeste       | probable<br>SNF2 hel            | two-comp      | hypothet<br>hvpothet                     | sensor p       | sensor į                         | probable       | histidin           | hypothet       | DNA gyra       | transcri          | related        | probable       | hypothet       | aconitat       | hypothet       | hypothet       | probable          | DNA topo       | late exp           | hypothet       | . ZC262.3        | dimethyl       | dimethyl              | hypothet       | hypothet       | probable       | leucine-       | virB4 pr      | virb4 pr      | DNA gyra       | phenylal           | DNA topo          | hypothet       | xylan 1,           | hypothet       | glucocor           | hypothet           |
| alanine-tRNA ligar<br>probable mmpL1 prot<br>hypothetical prot<br>hypothetical prot | ālyl tRNA syntheta<br>valine-tRNA ligase<br>probable membrane | penicillin-bir<br>progesterone r | rep-1 protein, | hypothetical prote | progesterone r | probable ligar<br>SNF2 helicase | two-component | hypothetical prote hypothetical prote    | sensor protein | sensor proteir<br>hypothetical n | probable ligar | histidine kina     | hypothetical p | DNA gyrase, ch | transcription     | related to tra | probable 2-com | hypothetical p | aconitate hydr | hypothetical p | hypothetical p | probable membr    | DNA topoisomer | late expression fa | hypothetical p | . ZC262.3 protei | dimethylglycin | dimethylalycin        | hypothetical p | hypothetical p | probable membr | leucine-tRNA l | virB4 protein | virb4 protein | DNA gyrase sut | phenylalanine-tRNA | DNA topoisomerase | hypothetical p | xylan 1,4-beta-xyl | hypothetical p | glucocorticoid rec | hypothetical prot  |

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hypothetical protein T27F4.12 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change C;Accession: A96689 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: B96689

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: B96689
                                                                                                                         A96689
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-139 <STO>
A; Cross-references: GB: AEO05173; NID: g10092496; PIDN: AAG12896.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T27F4.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Aug-2002
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                              Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                              C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
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                               Alonso,
war, K.;
                                                                                                                                                                       myb-related transcription factor MYB75 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000 C:Accession: T51680
 A;Status: preliminary; translated from GB/EMBL/DDB
A;Molecule type: mRNA
A;Residues: 1-212 <KRA>
A;Cross references: EMBL:AF062908; PIDN:AAC83630.1
A;Experimental source: cultivar Columbia
                                                                           R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51680
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H.; Kranz, H.D.;

Denekamp, M.;

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A;Cross-references: C
C;Genetics:
C;Gene: T27F4.12
A;Map position: 1
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C;Superfamily:
C;Keywords: tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Reture: Preliminary

A;Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                   myb-related transcription factor MYB90 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51687 R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.;
                                                                                                                                                                                                                        A;Cross-references: EMBL:AF062915; PIDN:AAC83637.1
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-249 <KRA>
                                                                                                                                                                                                                                                                                                                                                                   Paz-Ares, J.; Weisshaar, B.

Plant J. 16, 263-276, 1998

A;Title: Towards functional characterisation of the mer
A;Reference number: Z14349; MUID:9839469; PMID:9839469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
T51687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-246 <STO>
                                                                                                                                                                                                                                                                                                                                                  A; Accession: T51687
                                                                               Best Loc
Matches
                                                                                                                                                                  Superfamily: Arabidopsis 28K leaf-specific; Keywords: transcription factor
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Best Local
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75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                               Similarity
32; Conserv
                                                                                                                                                                transcription
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                   LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRIHKLIGNRWSLIAGRIPGRTANDVKNYWNT
  LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                 Conservative
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                                                                                                    11.7%;
100.0%;
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;; Pred. No. 2.2:
0; Mismatches
                                                                               0;
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Pred. No.
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                                                                                 Mismatches
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2.2e-26;
                                                                                                    DB 2;
2.3e-
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                                                                                                                                                                                    protein; myb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.; Khaykin, E.; Kim, C.:
.S.; Maiti, R.; Marziali,
                                                                                 ç,
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                                                                                                                                                                                                                                                                                                                                                                                               R2R3-MYB gene from
                                                                                 Gaps
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                                                                                                                                                                                        DNA-binding
                                                                                 0
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T. Ker, M.; Wu, D.; Yu; G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; pMID:11130712
                                                                                                                                                                                                                                                                                     R;Loguercio, L.L.; Zhang, J.; Wilkins, T.A. submitted to the BMBL Data Library, November 1997 A;Description: Structure and expression of six classes A;Reference number: Z16842
                                                                                                                                                                                                                                                                                                                                                                               C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C;Accession: T09744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription factor F25P12.92 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: B96608
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C;Keywords: transcription
                                           A;Gene: Cmy-G
C;Superfamily: unassi
C;Keywords: DNA bindi
F;62-112/Domain: myb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005173; NID:g9954749; PIDN:AAG09100.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ansen, N.F.; Hughes, B.; Huizar, Nature 408, 816-820, 2000
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                                                                                                                                     A; Experimental C; Genetics:
                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                   A; Residues: 1-193 <LOG>
                                                                                                                                                                                                                                                                     A; Accession: T09744
                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: MYB-like DNA-binding domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myb-related protein - upland cotton
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Best Local S
Matches 27
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Best Local S
Matches 27
                                                                                                                                                     Cross-references: EMBL:AF034131; NID:g2921333; PID:g2921334
Experimental source: cultivar Acala SJ-2; ovule
    Query Match
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                                                                                       unassigned myb DNA-binding repeat proteins;
                                                                    binding; transcription regulation
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                                             DNA-binding
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    9.1%;
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                                           repeat homology <MYB>
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Pred. No.
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Pred. No.
    Score 25;
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5.8e-21;
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5e-21;
    DB 2;
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Length 193;
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                                                                                         DNA-binding
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                                                                                         repeat homol
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A;Cross-references: EMBL:AF015269; NID:g2343274; PIDN:AAB67721.1; PID:g2343275
A;Experimental source: cultivar W22
A;Note: the protein is nonfunctional due to insertion of retrotransposon Magel C;Genetics:
A;Gene: Pl
                                                                                                                                                                                                                                                                                                                                                                 x; Cooper, P.S.; Kent, B.; Matz, E.C.; Cone, K.C.
submitted to the EMBL Data Library, July 1997
A; Description: P1-987: a nonfunctional maize anthocyanin
A; Reference number: Z14257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T01189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-198 <LOS
A;Cross-references: EMBL:AF034130; NID:g2921331; PID:g2921332
A;Experimental source: cultivar Acala SJ-2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myb-related protein - upland cotton
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C;Accession: T09743
                                                                                                                                               A;Introns: 34/1; 77/2
C;Superfamily: anthoc;
F;51-101/Domain: myb W
                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-256 <C
                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T01189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Zea mays
C;Date: 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anthocyanin biosynthesis regulatory protein Pl, N;Alternate names: Pl transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Cmy-D
C;Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homolog
C;Keywords: DNA binding
F;63-113/Domain: myb DNA-binding repeat homology <MYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T09743
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1997 A;Description: Structure and expression of six classes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Loguercio, L.L.;
                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                        Matches
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Best Local
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                                                                                                          Query Match
                                                                                            Local
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                                   79 RIHKLIGNRWSLIAGRIPGRT 99
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                                                                                                                                                                                                                                                                                                    1-256 <COO>
                                                                                            Similarity
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                                                                                                                                               anthocyanin biosynthesis n: myb DNA-binding repeat
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                                                                        Conservative
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Pred. No.
                                                                                            Score 21;
Pred. No.
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89
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                                                                                                           DB 2;
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C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T03974
R;Cone, K.C.; Cocciolone, S.M.; Moehlenkamp, C.A.; Weber, T.; Drummond, B.J.
Plant Cell 5, 1807-1816, 1993
A;Title: Role of the regulatory gene pl in the photocontrol of maize anthocy A;Reference number: Z15034; MUID:94138244; PMID:8305873
A;Accession: T03974
A;Status: preliminary; translated from GE/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-264 <CON>
A;Residues: 1-264 <CON>
A;Residues: 1-264 <CON>
A;Reperimental source: Strain Tx303
C;Genetics: (71.00/2)
  C;Specie
C;Date:
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C;Function:
C;Function:
A;Description: transcriptional activator for anthocyanin biosynthesis
A;Description: transcriptional activator for anthocyanin biosynthesis
C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-bi
F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
F;62-112/Domain: myb DNA-binding repeat homology <MYB1>
                                                                                  RESULT
T01188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T03972
R;Cone, K.C.; Cocciolone, S.M.; Moehlenkamp, C.A.; Weber, T.; Drummond, B.J.Plant Cell 5, 1807-1816, 1993
                                                                                                                                                                                                                                                                                                                                         A;Description: transcriptional activator for anthocyanin bic C;Superfamily: anthocyanin biosynthesis regulatory protein; F;9-61/Domain: myb DNA-binding repeat homology <MYB>F;62-112/Domain: myb DNA-binding repeat homology <MYB1>
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A;Gene: pl
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A; Residues: 1-266 < CON>
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                                         N;Alternate names: Pl
                                                            anthocyanin biosynthesis regulatory
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Best Local S
Matches 21
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    ;Species: Zea mays
;Date: 12-Feb-1999
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#sequence_revision 12-Feb-1999 #text_change 13-Aug-1999
                       (maize)
                                         transcription
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Pred. No.
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2e-14;
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A;Description: transcription regulation; stimulates expression of genes involved in anthoropy content of the co
R;Kranz, H.D.; Denekamp, M.; Paz-Ares, J.; Weisshaar, B. Plant J. 16, 263-276, 1998
                                                                                      probable transcription factor MYB82 [imported] - Arabidopsis thaliana (frag
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: transcriptional activator for anthocyanin biosynthesis C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-binding F;9-61/Domain: myb DNA-binding repeat homology <MYB> F;62-112/Domain: myb DNA-binding repeat homology <MYB1>
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C;Genetics:
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T03715
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A;Experimental source: cultivar
C;Genetics:
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A;Accession: T01188
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Description: Pl-987: a nonfunctional maize anthocyanin regulatory gene resulting from 1
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C; Function:
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A; Note: Pl-Bh (Blotchedl)
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A; Residues: 1-271 <C
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C;Date: 24
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A; Introns: 45/1; 8
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ce: cultivar W22
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Data Library, July 1997
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Pred. No.
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ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial C.A.; Li, J.H.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
S71287
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C; Accession: F96734
R; Theologis, A.; Ecker, J.R.; Palm,
R; Theologis, A.; Conn, L.;
                                                                                                                                                                                                                              R;Kirik, V.; Baumlein, H.
submitted to the EMBL Data Library, December 1995
A;Description: Isolation and chromosomal localization of leaf-specific cDNA encoding
                                                                                                                                                                                                                                                                                                                               myb-related 24.7K transcription factor - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 16-Jun-2000
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A;Accession: T51684
R;Kirik, V.; Baeumlein, H.
Gene 183, 109-113, 1996
A;Tille: A novel leaf-specific myb-related protein with a
A;Reference number: JC5729; MUID:97149286; PMID:8996094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 1
C;Superfamily: Arabidopsis myb-related 24.7K protein; myb DNA-binding
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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                                                                                             A;Residues: 1-213 <KIR>
A;Cross-references: EMBL:Z68157; NID:g1197189; PIDN:CAA92280.1;
                                                                                                                                                                                                                                                                                                               C; Accession: S71287; JC5729
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A;Accession: F96734
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;Residues: 1-130 <KRA>
;Cross-references: EMBL:AF062912;
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A;Accession: JC5729
A;Accession: JC5729
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-213 -KII2>
A;Cross-references: EMBL:Z68157; NID:g1197189; PIDN:CAA92280.1; PID:g1197190
A;Cromment: This protein is involved in the control of anthocyanin biosysthesis and the
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                                                                                                                                                                C;Superfamily: Arabidopsis myb-related 24.7K protein; myb DNA-binding repeat homology C;Keywords: DNA binding; nucleus; transcription regulation F;30-80/Domain: myb DNA-binding repeat homology <MYB2> F;54-80/Region: helix-turn-helix
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52 LLGNRWSLIAGRLPGRT
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ilarity 100.0%;
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68
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mycobacteri borrelia bu methanococc clostridium

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9 thermotoga
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lactococcus candida alb

Result No. Minimum Maximum Title: Perfect score: Scoring table: Database : Post-processing: Listing first 1000 Total number of hits satisfying chosen Word gize : Searched: OM protein -9 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. DB DB Score seq length: 0
seq length: 2000000000 protein search, using sw Query Match OLIGO Gapop 60.0 , Gapext 60.0 US-10-033-190-2 274 January 29, 2004, 20:13:57; Search time 18 Seconds (without alignments) 715.851 Million cell updates/sec 127863 seqs, 47026705 residues 0 SwissProt\_41:\* MNSTSMSSLGVRKGSWTDEE.....QQGVQNDDFSAEIDLWNLLD Copyright Length GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. DB MYBD MAIZE
TT2 ĀRATH
MYBC MAIZE
GL1 ĀRATH
MYB1 HORVU
MYBP MAIZE
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MARP ECOLI
PSB2 CRYNE
MYB3 HORVU
YAAC BACSU
MDHC HUMAN MYB2\_PHYPA
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KPYK LACLA
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p44845 haemophilus
p31802 escherichia
000826 cryptococcu
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| 1 SPEC STREY 1 APHA MORMO 1 PCNA SOYBN 1 PUR7 RICCN 1 PUR7 RICCN 1 PODCA 1 FODCA 1 FODCA 1 FOM PODCA 1 FOM HORSE 1 YSAS HUMAN 1 TPM HUMAN 1 TPM AMA 1 TPM AM | CASI_CAVPO  YRBI_YEAST  YT16_CAEEL  MINC_THEMA  TRAI_AGRTS  CF51_HUMAN  HIS1_AQUAE  KAD_CLOAB  HIS5_BRUME  HIS5_BRUME  HIS5_RHILO  TIMI_RAT  Y132_NPVAC  Y132_NPVA | 1 TPCH HOME 1 TPCB HOME 1 TPCB HOME 1 TYRE HOME 1 YNS EARN 1 Y28 VIBCI 1 Y208 VIBCI 1 Y207 WYCGI 1 GERD BACSI 1 LPCA METIJ 1 PTH CHLTE 1 Y293 BUCA. 1 Y293 BUCA. 1 Z293 BUCA. | 1 Y710 HABII 1 YAYC_SCHPI 1 KDGL HABII 1 KDGL HABII 1 WG15 BDRDI 1 RS11 BORBII 1 RS11 BORBII 1 RK12 CLOBI 1 RK17 CDOBI 1 RK17 CDOBI 1 RK17 CTOBI 1 RL19 CLOBI 1 RL19 CLOBI 1 YSMA BACSI 1 YSMA BACSI 1 DTD AQUAB 1 PCAI CANA 1 FCAI CANA 1 |
| <b>рн</b> 202 <b>н</b> 2202к                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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P18732 Q9Y0a7 P04656

P47303 P16450 Q58731 Q8kd05 P44905 P57136

mycoplasma
bacillus su
methanococc
chlorobium
haemophilus
haemophilus
wenopus lae
drosophila

homo sapien
buchnera ap
laquifex aeo
lescherichia
variola vir

Q9Cj30 P06708 P06708 P29290 P29293 P34598 P34598 P21797 Q9k184 Q9k186 P20963 P34601 P20963 P57663 P57663

balanus nub vibrio chol

mus musculu caenorhabdi bontastacus
homarus ame
homarus ame
bacteriopha
caenorhabdi

P41920 Q10919 Q9x0d7 P33907

thermotoga agrobacteri

saccharomyc caenorhabdi

Q00688 Q62446 Q79551 Q8p3y6 P59441 Q13493 P13380 Q59544 P22177

dinodon sem xanthomonas lactobacill

homo sapien

Q9wzg8 O46638 Q97114 P26884

P24730

1 homo sapien
3 aquifex aeo
9 clostridium
5 brucella me
5 rhizobium 1
0 rattus norv
0 autographa
8 thermotoga
8 oryctolagus
4 sulfolobus
4 bos taurus

Q969f1 067543 Q97ej9 Q8ye35 Q8gct5 Q98ct5

P44656 P41114 Q03975 Q9z810 P02561 P07226 P09495 P41277 Q60392

saccharomyc
methanococc

Q921x6 005946

3 neurospora
6 streptococc
4 morganella
7 glycine max
7 rickettsia
6 rickettsia
6 rickettsia
6 rickettsia
6 rickettsia
6 rickettsia
6 rickettsia
7 podocoryne
6 lytechinus
6 chlamydia p
6 equus cabal
8 homo sapien
8 rattus nory

| Fig. 1985   1987   1987   1988   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   1989   19   | 1113<br>1114<br>1115<br>1116<br>1117<br>1117<br>1117<br>1117<br>1117<br>1117                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 107<br>108<br>109<br>110<br>111                                                                                              |
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| The Court      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                              |
| ### 1007 CHANGE   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                              |
| 180   2.2   377   Y704_NETUN   2511   180   2.2   377   Y704_NETUN   2511   180   2.2   378   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180   2.2   381   180      | $oldsymbol{\cdot}$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | GPP2<br>TRPC<br>TRPC<br>NFU1<br>Y683<br>Y538                                                                                 |
| 8 2.2 377 1 Y704 METLY 8 2.2 382 1 PSS_SIREP 8 2.2 382 1 PSS_SIREP 8 2.2 385 1 REGE_VIECH 8 2.2 386 1 REGE_VIECH 8 2.2 386 1 REGE_VIECH 8 2.2 386 1 REGE_MYCTU 9 295268 8 2 387 1 EMRK ECOLI 9 295268 8 2 2 387 1 EMRK ECOLI 9 295268 8 2 2 387 1 EMRK ECOLI 9 22 387 1 EMRK ECOLI 9 22 397 1 PREF_SORMA 9 20 397 1 PREF_SORMA 9 20 397 1 PREF_SORMA 9 20 397 1 METK_STRAM 9 20 397 1 METK_STRAM 9 20 397 1 PREF_SORMA 9 20 398 1 METK_STRAM 9 20 399 1  | Q43124 brassica na P17070 oryza sativ O82797 nicotiana t O96yw0 sulfolobus O99k84 chlamydia m Q02150 lactococcus P53997 drosophila P75792 escherichia P75792 escherichia P75792 escherichia P75792 escherichia P75792 escherichia P75792 escherichia P75793 lomo sapien P71107 mus musculu P71850 mycobacteri P42182 bacillus su P71850 mycobacteri Q91jd0 mus musculu Q47921 mastigoclad Q9br69 paremophilu P51613 vitis vinif Q64662 spermophilu P64662 spermophilu P75300 mycoplasma Q96ck4 homo sapien P51513 vitis vinif Q64662 spermophilu P76256 hydra atten P75300 mycoplasma Q96ck4 homo sapien P517010 pacudomonas P51700 rattus norv Q9swh4 arabidopsis P21726 pisum sativ Q9sw14 pyrococcus Q9sw14 promisetum P57566 buchnera ap Q09204 caenorhabdi Q47100 pseudomonas P51700 buchnera ap Q09712 sulfolobus Q9m712 sulfolobus Q9m712 streptococc Q9sy14 str | saccharon<br>listeria<br>listeria<br>listeria<br>saccharor<br>methanocc                                                      |
| 2.2 377 1 Y704 METJA OSBITS 2.2 387 1 PSJ SHEEP 2.2 386 1 PROFE MICHIN OSSBEE 2.2 386 1 PROFE MICHIN OSSBEE 2.2 386 1 PROFE SORMA 2.2 397 1 METK STRAM 2.2 401 1 DOCD SALITY 2.2 401 1 DOCD SA | 186 188 189 199 199 199 199 199 199 200 200 200 200 200 200 200 200 200 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 180<br>181<br>183<br>184<br>185                                                                                              |
| 2 377 1 Y704 METUA 058115 2 387 1 PAGE VIECH 2 388 1 PAGE VIECH 2 398 1 PAGE PARNO 2 398 1 PAGE PARNO 2 399 1 PAGE PAGE 2 397 1 PAGE PAGE 2 397 1 PAGE PAGE 2 397 1 PAGE PAGE 2 399 1 PAGE 2 399 1 PAGE 2 399 1 PAGE PAGE 2 399 1 PAGE 2 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                              |
| 1 Y704 METJA Q58115 1 ARGE VIECH 1 ARGE VIECH 2 P53 SHEEP 2 P53 SH |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                              |
| Y704 METJÄ ARGE VIBCH PS3 SHEEP PS3 SHEEP PS3 SHEEP PS4 SHOLL RECF MYCTU Q29528 REAR ECOLI PS53 BOVIN Q29628 REAR ECOLI PS53 BOVIN Q29628 REAR ECOLI PS53 BOVIN Q29628 REAR ECOLI PS53 BOVIN Q36006 Q31677 AAT1 BACGU CAT1 RESULA PS3 MARMO Q36006 Q31677 AAT1 BACGU PS3 MARMO Q36007 Q31677 AAT1 BACGU PS3 MARMO PS3001 XYLH ECOLI PS5 STRHY PS5001 XYLH ECOLI PS5 STRHY RETK STAAM RETK SCHPO RETT SCHPO R |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                              |
| Q58115 methanococc Q9knt5 vibrio chol P51664 ovis aries Q59528 bos taurus Q59528 bos taurus Q59529 escherichia Q12624 humicola in Q3606 marmota mon Q91677 xenopus lae P5307 staphylococ Q81729 staphylococ Q81729 staphylococ Q81729 staphylococ Q81729 avian serce Q99779 staphylococ Q81720 avian serce Q99779 avian serce Q99779 lomo sapien Q81720 avian serce Q99779 lactococcus Q81720 avian serce Q99779 lactococcus Q81720 saccharomyc Q93561 ricketteila Q90729 lactococcus Q807460 nicotiana t Q90729 lactococcus Q8074700 saccharomyc Q90730 bacilus su Q90730 b | 22.22.22.22.22.22.22.22.22.22.22.22.22.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 2.2 377<br>2.2 378<br>2.2 382<br>2.2 385<br>2.2 386<br>2.2 386<br>2.3 387                                                    |
| רות או מודמו הממנו הממוחמים או אי מודמים במוחדים במוחדים במוחדים במוחדים במוחדים במוחדים במוחדים במוחדים במוחדים                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 22.22.22.22.22.22.22.22.22.22.22.22.22.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 2.2 377 1 Y704<br>2.2 378 1 ARGE<br>2.2 382 1 P53 0<br>2.2 385 1 REF<br>2.2 386 1 P53 0<br>2.2 386 1 P53 0<br>2.2 387 1 EMRK |

| 266<br>267<br>268<br>269<br>277<br>277<br>277<br>277<br>277<br>277<br>277<br>277<br>277<br>27                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                   |
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| α α α α α α α α α α α α α α α α α α α                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <b>あ</b> ,あ あ あ あ あ あ あ あ あ あ あ                                                                                                                                                                                                                                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                                                                          |
| $\begin{array}{c} 5.53 \\ 5.53 \\ 5.53 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.54 \\ 5.$ |                                                                                                                                                                                                                                                                                                          |
| ERUM ERUM ESCC FORET FOR                                                                                                                                                                                                                                                                                                                | PDI N<br>SHSI<br>Y369<br>Y167<br>YXAK<br>C11A<br>C11A<br>MALQ<br>UDBE<br>UDBE<br>INV1<br>INV1<br>INV4<br>YRR5<br>YRR5                                                                                                                                                                                    |
| Q8ye41 brucella me Q8ye41 brucella me Q8ye5 brucella su Q99829 bomo sapien P30986 eschscholzi P30614 yarrowia li Q95547 thermoplasm P49425 thermoplasm P49426 arabidopsis P73866 synechocyst P42770 arabidopsis P73866 synechocyst P42770 arabidopsis P73866 synechocyst P42771 drosophila P56721 drosophila P56721 drosophila P56721 drosophila P56721 thermoactin P38289 saccharomyc P34802 caenorhabdi P4783 saccharomyc P34140 drosophila P36202 human papil Q9zm93 helicobacte Q80902 human papil Q9zm93 helicobacte Q81440 drosophila Q9de137 mus musculu Q9hj89 thermoplasm P04197 drosophila P31636 sus scrofa P31636 sus scrofa P40002 saccharomyc Q01159 chlorella v Q94769 homo sapien P23327 homo sapien P232                                                                                                                                                                                                                                                                                                                | P52588 zea mays (m<br>P97797 m protein-t<br>O83384 treponema p<br>P40492 saccharomyc<br>Q21973 caenorhabdi<br>Q9q282 mus musculu<br>Q9pku9 chlamydia m<br>P36513 oryctolagus<br>P10594 saccharomyc<br>P10596 saccharomyc<br>Q09346 caenorhabdi<br>Q8tta3 methanosarc<br>Q75375 mycoplasma                |
| ۵۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵ ۵                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 3333330098728<br>3343321                                                                                                                                                                                                                                                                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                                                                          |
| 752<br>752<br>753<br>754<br>755<br>757<br>757<br>757<br>757<br>757<br>757<br>757<br>757                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 717<br>723<br>723<br>723<br>728<br>738<br>734<br>736<br>736<br>750<br>750                                                                                                                                                                                                                                |
| MENT YEAST MENT HUMAN GSH1 PASMU YURA CHICK METE SOLSC METE ARATH BCSB SALITI BCSB SALITI BCSB SALITI BCSB SALITI GCR AOTNA GCR SAIBB THETN TRAY THATN GYBA BACHD SYLB CAMJE TRAY TAXBR TRAY TAXBT HUMAN NAHS                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                          |
| P006 P00 P20 P20 P20 P20 P20 P20 P20 P20 P20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 000<br>000<br>000<br>000<br>000<br>000<br>000<br>000<br>000<br>00                                                                                                                                                                                                                                        |
| p32892 saccharomyc p10243 pasteurella p5250 gallus gallus gall (9314 caenorhabdi Q42662 solenostemo o50008 arabidopsis galmonella g3317 schizosacch p49115 cavia porce p34595 caenorhabdi p79686 actus nancy p04150 homo sapien p79269 sajminis lombor proce p34595 caenorhabdi p7668 actus nancy p1652 escherichia o60603 homo sapien p795m5 macaca fasc g8x518 escherichia o60603 homo sapien p1926 bacillus su p17922 bacillus su p17924 bacillus bacca q1594 taxus chine p17924 baccharomyc p1794608 scherichia p1794608 clostridium p1794608 clostridium p1794608 clostridium p1794608 clostridium p1794608 accharomyc p1794609 accharomyc p179                                                                                                                                                                                                                                                                                                                | 2225 xenopus lae<br>k078 mus musculu<br>9n01 rattus norv<br>9n01 rattus norv<br>2755 homo sapien<br>4312 drosophila<br>1640 pinus thunb<br>103v8 drosophila<br>103v8 drosophila<br>103v8 rattus norv<br>2637 neurospora<br>5431 rattus norv<br>1774 mycobacteri<br>19140 gallus gall<br>1960 mus musculu |

| 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 44444440000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 399<br>400                                                      |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|
| ம <b>் மா மா மா கை க</b> ை கை                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ Თ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | νοο                                                             |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 958<br>958<br>959<br>971<br>971<br>971<br>972<br>1102<br>1102<br>1102<br>1102<br>1102<br>1102<br>1102<br>11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | MALI_MYCTU SYAC_YEAST 1 YAX6_YEAST 1 YAX6_YEAST 1 YAX6_YEAST 1 YEAST 1 |                                                                 |
| human par<br>buman par<br>plasmodiu<br>herpesvii<br>homo sapi<br>rattus no<br>bos tauru<br>m inosico<br>rattus no<br>homo sapi<br>plasmodiu<br>gallus ga<br>homo sapi<br>homo sapi<br>homo sapi<br>homo sapi<br>penaeus no<br>candida a<br>pichia pa<br>methanoge<br>papio ham                                                                                                                                                                                                                                                                                                                                             | ycobacter accharomy accharomy accharomy orrelia by ycoplasma accharomy hlamydia accharomy hlamydia accharomy hlamydia accharomy ctinobaci ctinobaci ctinobaci ctinobaci chizosacc actus muscul chizosacc actus muscul crishinancaci chi scherichi scherichi scherichi scherichi scherichi scherichi scherichi sacillus muscul eishinania attus nor sapie omo sapie omo sapie omo sapie omo sapie ersinia e genome sapie ersinia e genome sapie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | chlamydia<br>saccharom                                          |
| 521<br>522<br>522<br>522<br>522<br>523<br>523<br>523<br>533<br>533<br>533                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 55116<br>5116<br>5116<br>5116<br>5116<br>5116<br>5116<br>511                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 472<br>473                                                      |
| ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ੶<br>ຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑຑ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | រាហាហា                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1 1 1<br>2 60 60                                                |
| 888888778666666666683118880088888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 79888886666633366666557555446                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 41<br>43                                                        |
| VF07  AKA7  DBHL  DBHL  CY2 B  VS1 B  VG73  VG73  VG73  VG73  VG73  VG73  VG73  VG73  VG73  RS16  Y706  Y706  ACP C  GOVPA  ACP C  VG73  VG73  VG73  VG73  VG73  VG73  RS16  RS16  RS16  RS16  RS16  RS15  RS15  RS15                                                                                                                                                                                                                                                                                                                                                                                                      | RS7_SALSA  1 RS7_SALSA 1 Y476 HABIN 1 Y476 SYNY3 1 Y499 SYNY3 1 MT CHICK 1 MORI BOMMO 1 WARL BOMMO 1 WARL BOMMO 1 WAS THERE 1 YUGA VACCC 1 YUGA WACCC | 1 UR1_CATCO 1 MTA_COLVI                                         |
| P33867 variola vir O55074 mus musculu Q92h14 rickettsia Q92d26 borione resp P22995 escherichia p00097 rhodocyclus Q05288 mycobacteri Q05288 mycobacteri Q05288 mycobacteri Q05288 mycobacteri Q05288 mycobacteri Q05288 mycobacteri D1921 concorhynchu Q68680 bacillus me Q51638 borrelia bu P03793 bacteriopha Q90clq3 pasteurella Q956135 mus musculu p07420 dasyurus vi Q96cb4 mus musculu p07420 dasyurus vi Q96cb4 mus musculu Q9hkn1 thermoplasma Q9mcq0 cenothera h P46189 mycoplasma P31529 sarcophaga | p47839 salmo salar p47839 salmo salar p47839 salmo salar p484002 haemophilus p344002 haemoplasm p74805 synechocyst p18018 clostridium p57912 pasteurella Q8yGy6 anabaena sp p23039 sulfolobus p258191 sulfolobus p58191 sulfolobus p58191 sulfolobus p58191 sulfolobus p15787 columba liv p09576 gallus gall p19279 thermoprote p82818 bombyx mori p36659 bombyx mori p366678 capterichia vi p3670 columba liv p095780 thermoplasm p3799 variola vi p30670 homo sapien p58086 thermoplasm p48504 solanum tub p36200 escherichia vi p30670 homo sapien p58086 thermoplasm p48504 solanum tub p30670 homo sapien p58086 thermoplasm p48504 solanum tub p30670 homo sapien p580850 treponema papil p3550 treponema papil p3550 treponema papil p3550 treponema papil p3550 secherichia p165239 homo sapien p04006 mus musculu p50238 homo sapien p04006 mus musculu p650318 there ia in p49214 nicotiana t p066478 aquifex aeo p083122 treponema p p08d2f1 wiggleswort p05813 listeria in p49214 nicotiana t p066478 aquifex aeo p083122 treponema p08d2f1 wiggleswort p05837 diaetoriana t p066478 aquifex aeo p083122 treponema p08d2f1 wiggleswort p0818747 methanobact p867677 chaetosphae                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | P01145 catostomus<br>P27086 collinus vir<br>P77087 collinus vir |

| 610<br>611<br>612<br>613<br>614<br>615                                                                                              | 6008<br>6008<br>908  | л б б б б б<br>6 0 0 С<br>7 4 С<br>7 В | 599<br>599<br>599    | 595<br>596                    | 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 5 5 5 6<br>5 6 6<br>5 7 6 6 | 587<br>588            | 585<br>586<br>586                                             | 582<br>583                                                     | 579<br>580               | 576<br>577                               | 573<br>574      | 570<br>571<br>572                     | 568<br>569     | 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 563<br>564               | 561<br>61          | 5 5 5 6<br>5 6 6 | 557<br>557               | ນ (ນ (<br>ນ (ນ ( | л 55<br>7 53<br>7 64 | 551<br>552 | 549<br>550               | 547<br>548                                   |
|-------------------------------------------------------------------------------------------------------------------------------------|----------------------|----------------------------------------|----------------------|-------------------------------|---------------------------------------|-----------------------------|-----------------------|---------------------------------------------------------------|----------------------------------------------------------------|--------------------------|------------------------------------------|-----------------|---------------------------------------|----------------|-----------------------------------------|--------------------------|--------------------|------------------|--------------------------|------------------|----------------------|------------|--------------------------|----------------------------------------------|
| រាហេហហហហហហ                                                                                                                          | ហេហហហប               | <b>ភហហហ</b> បាប                        | រាហហហ                | ហហហ                           | າທະທະບ                                | ហហហប                        | រាហហ                  | ហហប                                                           | ហហហ                                                            | ហហប                      | n ហា ហា (                                | រាហៈហៈ          | <b>ர</b>                              | տտ             | n ហ ហ                                   | ហហ                       | лunu               | <b>ո</b> Մո (    | ли                       | лυι              | ற போ                 | ທ ທ        | ហហ                       | ហហប                                          |
| 1111111                                                                                                                             |                      |                                        |                      |                               |                                       |                             |                       |                                                               |                                                                |                          |                                          |                 |                                       |                |                                         |                          |                    |                  |                          |                  |                      |            |                          |                                              |
| 105<br>106<br>107<br>107<br>107                                                                                                     |                      |                                        |                      |                               |                                       |                             |                       |                                                               |                                                                |                          |                                          |                 |                                       |                |                                         |                          |                    |                  |                          |                  |                      |            |                          |                                              |
| 1 YDO1 RICCN 1 CO7S_HUMAN 1 YFD2 YEAST 1 FER BUCBP 1 PRVZ_SALSA 1 PRVB_ESOLU 1 THIO_CLOLU                                           |                      | YN4<br>HSP<br>THI                      | HSP3<br>RS24<br>VGES | GTH<br>HBA                    |                                       |                             | PD1                   | PD11                                                          |                                                                |                          | RECTION                                  | VPR I           | S11<br>S11<br>VE7                     |                | RL31                                    | RL31                     | FANA               | RS19_            | RS19_                    | KPYK             | IM10                 | TRP6       | GATC<br>PSK1             | 1 1874 CAUCK<br>1 YYCC BACSU<br>1 AP21 HUMAN |
| Q92924 rickettsia 060397 homo sapien P43566 saccharomyc Q89a15 buchnera ap Q91483 salmo salar P02619 esox lucius P21609 clostridium | trep<br>homo<br>ther | archae<br>archae<br>rattus<br>dictyo   | hai                  | human p<br>thunnus<br>mesocri | homo s                                | haemophil<br>cyanidium      | ans<br>ans            | P30787 rhodobacter<br>P56982 bos taurus<br>Ogyfor homo sanien | Q02272 pygmy chimp<br>Q05251 mycobacteri<br>P95516 pasteurella | X UT H                   | Q8pu21 methanosarc<br>Q92fr6 listeria in | human<br>rhizol | P08206 homo sapien P27004 xenopus lae | carica         | pyro                                    | pyroc                    | P07104 escherichia | neiss            | buchnera a               | candida al       | neurospora           | rick.      |                          | baci.                                        |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                               | 682                  | 675<br>676<br>677                      | 671<br>672<br>673    | 668<br>669<br>670             | 666<br>667                            | 6663<br>6633                | 660                   | 657<br>658                                                    |                                                                | 652                      | 6549                                     | 645<br>647      | 644<br>644                            | 641            | 639<br>639                              | 636<br>637               | 634                | 632              | 630                      | 628              |                      | 624<br>625 | 622<br>623               | 620<br>621                                   |
| កហហហហហហ                                                                                                                             | ហេហហេហ               | កហហហហ                                  | n ហ ហ ហ              | ហហហ                           | ហេហប                                  | ហេហប                        | ոտտ                   | ហហ                                                            | ហហហ                                                            | თ თ i                    | יטיטי                                    |                 | រាហាហា                                | ហហប            | יטיטי                                   | ហហ                       | กเกเ               | n UT U           | กเกเ                     | าเกเ             | ាហៈប                 | лon        | ហហ                       | រាហប                                         |
|                                                                                                                                     | 1.000                | 11.8                                   | 1111<br>088          | 1.8                           | 11.8                                  | 11.6                        |                       | - <u></u>                                                     | 11.8                                                           | 1.00                     |                                          |                 | 1.1.0                                 | 1 1 .<br>8 8 0 |                                         |                          |                    |                  |                          | 1.8              | . 60 0               | 9 8 R      | 1.8                      |                                              |
|                                                                                                                                     | 125<br>125<br>126    |                                        |                      |                               |                                       |                             |                       |                                                               |                                                                |                          |                                          |                 |                                       |                |                                         |                          |                    |                  |                          |                  |                      |            |                          |                                              |
|                                                                                                                                     |                      |                                        |                      | 111                           |                                       |                             |                       |                                                               |                                                                |                          |                                          |                 |                                       |                |                                         | $rac{1}{2}$              |                    |                  |                          |                  | ٠ ٣ ٠                | <b>-</b>   |                          |                                              |
| 26 1 RECX_HAEIN 26 1 RECX_HAEIN 27 1 YCBK HAEIN 29 1 RY2F HUMAN 29 1 RRB NEPOL 29 1 TKNI HUMAN 29 1 TKNI HUMAN 30 1 TKNI Z-DANTH    |                      |                                        |                      |                               |                                       |                             | WNT6_EVATR            | YCFF HAEIN<br>CHH3 PENJP<br>V03 RPT7                          | YA9D_SCHPO<br>SMS_CHICK<br>Y1B_SOCMV                           | SMS1_RANRI<br>TKN1_RABIT | Y076 METJA<br>IFIA PYRAE                 |                 |                                       |                |                                         | PRVB_OPSTA               | PRVA_RAT           | PRVA_MACFU       | PRVA_GERSP               | Y11K_PASVK       | PRVB_MERBI           | PRVB_CYPCA | PRVA_ESOLU<br>PRVB_AMPME | PRVA_BRARE                                   |
|                                                                                                                                     |                      |                                        |                      |                               |                                       |                             | WNT6_EVATR WNT6_STRPU | YCFF HAEIN<br>CHH3 PENJP<br>VO3 RPT7                          | YA9D_SCHPO<br>SMS_CHICK<br>Y1B_SOCMV                           | SMS1_RANRI<br>TKN1_RABIT | YOF METUA<br>IFIA PYRAE                  |                 |                                       |                |                                         | PRVB OPSTA<br>PRVU CHICK | PRVA_RAT           | PRVA_MACFU       | PRVA_FELCA<br>PRVA_GERSP | Y11K_PASVK       | PRVB_MERBI           | PRVB_CYPCA | PRVA_ESOLU<br>PRVB_AMPME | ONCO_HUMAN PRVA_BRARE PRVA_CYPCA             |

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| ាហហហហ                                                                                           | រហេហ                                                                        | ரைமு                                     | រាហប                                                           | រហេប                                    | ាហាហ                                          | лип                | ហហ                                       | տ տ                                           | տ տ                                        | ហេប                | រា ហ្រ              | տ տ                                     | ທ ທ                         | יטינ                          | лUn                 | ហយៈ                                   | ហហ                                       |                                         | лυ                  | ຫ ຫ                                          | տ տ                | ហហ                                       | տ տ                                      | ທ ທ                                      | υ (<br>,           | лuп                | ഗ ഗ                                        | ı UT U            | лσ                  | տ ս                | лUп                | տ տ                                      | n Un                | ຫຸ ຜ                                       | ່ເທີບ             | າທ                 |
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| 156 1                                                                                           |                                                                             |                                          |                                                                |                                         |                                               |                    |                                          |                                               |                                            |                    |                     |                                         |                             |                               |                     |                                       |                                          |                                         |                     |                                              |                    |                                          |                                          |                                          |                    |                    |                                            |                   |                     |                    |                    |                                          |                     |                                            |                   |                    |
| ATPX ODOSI BFR SYNY3 COAD PYRAB COAD STARP                                                      |                                                                             | Y406 CHLTR<br>YX2 CVHSA                  |                                                                |                                         |                                               | •                  |                                          |                                               |                                            |                    |                     |                                         |                             |                               | •                   |                                       |                                          |                                         |                     | ,                                            |                    |                                          |                                          |                                          |                    | •                  |                                            |                   |                     |                    | •                  |                                          |                     |                                            | HBG_HUMAN         | -                  |
| Q00823 odontella se Q00823 odontella se P24602 symechocyst Q9uyt0 pyrococcus Q8cmi0 staphylococ | paracocc<br>vibrio f<br>vibrio v                                            | 084411 chlamydia t<br>P59633 human coron | P54046 methanococc<br>Q9y3c5 homo sapien<br>O9qvk7 mus musculu | P15210 catostomus<br>Q9hhn3 halobacteri | P72080 neisseria m<br>P56276 meleagris g      | P56998 meisseria m | p38898 saccharomyc                       | Q871f7 vibrio para<br>O9pgv8 ureaplasma       | Q9z819 chlamydia p<br>Q9pjz0 chlamydia m   | P55502 rhizobium s | archaeog            | 044437 drosophila<br>026373 methanobact | mus i                       | P51638 rattus norv            | homo                | 014015 schizosacch P25908 synechococc | 084741 chlamydia t<br>09z729 chlamydia n | P47721 mycoplasma Ogolio chlamydia m    | homarus             | P33395 desulforibr<br>P29490 vibric chol     | Q9juw1 neisseria m | Q92bj1 listeria in<br>O66592 amuifex aeo | P05933 schizosacch<br>P20690 asterias am | Q09373 caenorhabdi<br>P58685 clostridium | P41369 staphylococ | Q9a8j3 caulobacter |                                            | P15211 catostomus | Q60280 methanococc  | Q45478 bacillus su | Q9blg0 todarodes p | Q9ydg2 aeropyrum p<br>O66475 aquifex aeo | , ∃                 | P02099 oryctolagus<br>P58208 escherichia   |                   | p08224 cheirogaleu |
| 979<br>978<br>980<br>981                                                                        | 974<br>975<br>976                                                           | 972<br>973                               | 970<br>971                                                     | 968                                     | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0         | 964                | 962                                      | 960<br>961                                    | 959<br>959                                 | 957<br>957         | 955                 |                                         |                             | 950                           | 948                 | 946                                   | 944                                      | 942<br>942                              | 940                 | 928                                          | 936                | 93.4                                     | 932                                      | 930<br>931                               | 929                | 927                | 925<br>926                                 | 924               | 922                 | 921                | 919                | 917<br>918                               | 916                 | 914<br>915                                 | 913               | 911                |
| ហេហហហប                                                                                          | រហេហហ                                                                       | மை                                       | ភហប                                                            | n ហ ហ                                   | ហ្រប                                          | ոտ                 | <b>சு ப</b> ொ                            | ຫຫ                                            | ហហ                                         | υιο                | ៣ហាប                |                                         | თ თ                         | ເທັບ                          | ni Un               | மை<br>ம                               | ກທເ                                      | ກທູ                                     | וטו                 | יטית                                         | თ თ (              | יוטית                                    | ທທ                                       | տ տ                                      | ហៈប                | лvī                | თ თ                                        | ហប                | n vi                | տս                 | n Un               | ர ர                                      | י טי                | ហហ                                         | <b>ரு</b> ர       | ı UT I             |
|                                                                                                 |                                                                             |                                          |                                                                |                                         |                                               |                    |                                          |                                               |                                            |                    |                     |                                         |                             |                               |                     |                                       | 1.8                                      | 1.6                                     | 1 1 1               | - 1-<br>20                                   | 200                | - L                                      | 1.8                                      | 1.8                                      | 1.8                | 1.8                | 1.8<br>1.8                                 | 1.8               |                     | 1.8                | 1.8                | 1.8                                      |                     | 1.8<br>8                                   | 1.8               | 1.8                |
|                                                                                                 |                                                                             |                                          |                                                                |                                         | <u>, , , , , , , , , , , , , , , , , , , </u> | <b>.</b>           |                                          |                                               |                                            |                    |                     |                                         |                             |                               |                     |                                       | , بر د                                   |                                         | ן ען ג              | ر بر د                                       | 111                | - 11                                     | 155                                      |                                          | ш,                 |                    |                                            |                   |                     |                    |                    |                                          | 1 1                 | 15                                         | 157               | 157                |
| 166                                                                                             | 166<br>166                                                                  | 165                                      | 165<br>165                                                     | 165                                     | 3 23 5                                        | 3 & 3              | 201                                      | 8.8                                           | 62                                         | 62                 | 162                 | 2 2                                     | 161<br>161                  | 161                           | 161                 | 161                                   | 99                                       | 200                                     | 000                 | 000                                          | 000                | 5 6                                      | 9                                        | 59                                       | 59                 | n is<br>0 0        | 5 6                                        | 158               | 58                  | 158                | 158                | 5 6                                      | 7                   | 7 7                                        |                   |                    |
| 166 1 YC93 CLOAB<br>167 1 MB12 MYCLE<br>167 1 T2DB YEAST<br>167 1 Y199 MYCGE                    |                                                                             |                                          |                                                                | 1 GCSH                                  | <b>,</b> , ,                                  | - μ,               |                                          |                                               |                                            | <b>-</b> -         |                     | <u>_</u>                                |                             | , <sub>1</sub> , <sub>1</sub> | ــر ــ              | <b>–</b> – ,                          | 1 MAX                                    |                                         | ر بر د              | <u>-                                    </u> |                    |                                          |                                          | р н                                      | μ,                 |                    | <b>-</b> -                                 | 1 RS19            | 1 GSH               | 1 FCY              | ـــ ــ             | 1 BFR                                    | 1 YMF               | 1 YBU                                      | Y93               |                    |
| . 4 4 4 4 4                                                                                     | 1 PMPB_CANBO P1429 1 VSNI_NOCAE P5018 1 V346_MYCGB P4758 1 V346_MYCGB P7525 | 1 YC89 METJA<br>1 PMPA CANBO             | 1 MAX_BRAKE P5216 1 PDA1_METMA P5888 1 PSAF_SYNY3 P2925        | 1 GCSH_DROME Q9u61                      | 1 Y057 NPVOP 01031 1 YAG5_SCHPO 00061         | 1 PTSN ECOLI P3122 | 1 MORE BRUME QBYGA<br>1 PHAC CYACA Q9tlw | 1 LEUD_PYRHO . 059393<br>1 MAX XENLA . 007016 | 1 YBFM_BACSU 031453<br>1 IPYR_STRCO Q9x8i9 | 1 RECX_XANOR       | 1 PTSN_KLEPN P17162 | 1 FIGA_AGRT5 Q44339                     | 1 TPM_SCHPO<br>1 YU12_CLOPE | 1 TPCC RABIT P02591           | 1 TPCC_HUMAN P02590 | 1 TPCC COTUA P05936                   | 1 MAX RAT                                | 1 MAX HUMAN P554134 1 MAX HOTIGE D28574 | 1 IAGE SALTY P43017 | 1 COAD_PYRFU QBULX0                          | 1 CNIL HUMAN       | 1 Y215_METUA Q57668                      | 1 BV1J_BETVE P43183 1 RIB4_SCHPO 0900b1  | 1 BV1E_BETVE P43178 1 BV1E_BETVE P43179  | 1 BFR_SERMA 068935 | 1 BFR MYCLE P43315 | 1 Y488_METJA Q57912<br>1 ATPX_ANTSP Q02852 | 1 RS19_PYRAE      | 1 GSHJ_SCHPO O59858 | 1 FCY1 YEAST       | 1 BTG2 RAT P27049  | 1 BFR_ECOLI P11056<br>1 BFR_SALTY O68926 | 1 YMFO_ECOLI P75980 | 1 YBUK_CLOBE Q05626<br>1 YF53_METJA Q58948 | Y935_AQUAE P50776 | MNBB MAIZE P27347  |

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       InterPro; IPRO01005; Myb DNA binding.
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"Molecular analysis of the C1-I allele
mutant of the regulatory C1 locus.";
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MEDLINE=90151603; PubMed=2303027;
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Nuclear protein;
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MISCELLANBOUS: THE C1-I ALLELE IS A DOMINANT NEGATIVE MUTANT WHICH INHIBITS PIGMENT FORMATION.
                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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regulatory C1-I protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stracke R., Werber M., Weisshaar B.; "The R2R3-MYB gene family in Arabidopsis thaliana."; Curr. Opin. Plant Biol. 4:447-456(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND MUTANTS TT2-2 AND STRAIN=cv. Columbia, cv. Landsberg erecta, MEDLLNE=211344722; Pubmedian T
This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                        +
                                                                                                                                                                                                                                                                                                                                                 physically assigned P1 and DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                                                                                                                     Sequence features
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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MEDLINE=21481677; PubMed=11597504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Cell 13:2099-2114(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis
                                                                                                                                                                                                          FUNCTION: Transcription factor involved in the cor flavonoid late metabolism in developing siliques. in determining the tissue-specific activation of leucoanthocyanidin reductase (BANYULS). SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Expressed at a high level in i and at a lower level in flowers. Undetected in you
                                                        SIMILARITY: Contains 2 Myb-like domains.
                                                                                            completion of MISCELLANEOUS:
                                                                                                                                roots, leaves and inflorescence stems.

DEVELOPMENTAL STAGE: Highly expressed from
of embryogenesis to the globular stage, dec
the late heart-torpedo stage and did not pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i N., Jond C., Debeaujon I., Caboche M.,
Arabidopsis TT2 gene encodes an RZR3 M.
key determinant for proanthocvanidin.
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                                                                                            embryogenesis. : TT2 activity
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MYB 2.
POLY-GLY:
AD61FA2B829C5FBD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T.,
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                  It is produced through
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DT 01-MAR-1989
DT 01-MAR-1989
DT 28-FEB-2003
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Matches 17
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VARIANT
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SMART; SN00717; SANT; 2.
PROSITE; PS00037; NYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                       Paz-Ares J., Ghosal D., Wienand U., Peterson "The regulatory c1 locus of Zea mays encodes to myb proto-oncogene products and with struc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PARCAD clade; Panicoldeae; Andropogoneae; Zea.
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EMBL; AF371981; AAK54744.1; -.
EMBL; AB015477; BAB08716.1; -.
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Bioinformatics an
                                                                                                                                                                                                                                                                                                               transcriptional activators.";
EMBO J. 6:3553-3558(1987)
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OJ. 6:3553-3558(1987).

FUNCTION: CONTROLS THE EXPRESSION OF AT LEAST 3 STRUCTURAL BIOSYNTHESIS. REGULATES THE EXPRESSION OF AT LEAST 3 STRUCTURAL GENUS: CHALCONE SYNTHASE, DIHYDROPLAVONOL REDUCTASE AND FLAVONOL O(3) GLUCOSYLTRANSFERASE. C1 ACTS AS A TRANS-ACTING FACTOR. SUBCELLULAR LOCATION: Nuclear (Probable).

SIMILARITY: Contains 2 Myb-like domains.
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174
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regulatory C1 protein.
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MISSING: IN TT2-2;
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ing; Repeat; Polymorphism.
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6.9e-10;
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Best Local S
Matches 17
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                                                                     MEDLINE=21396402; PubMed=11504855; Hauser M.T., Harr B., Schlotterer C.; "Trichome distribution in Arabidopsis Arabidopsis lyrata: molecular analysis GLABROUS1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
STRAIN=cv. Columbia;
MEDLINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Naka
                                                                                                                                                                                                            STRAIN=cv. Columbia;
MEDLINE=99449058; PubMed=10520748;
Shikazono N., Tanaka A., Yokota Y.
                                                                                                                                                                                                                                                                                   MEDLINE=92034971; PubMed=1934056;
MEDLINE=92034971; PubMed=1934056;
Oppenheimer D.G., Herman P.L., Sivakumaran
"A myb gene required for leaf trichome diff
is expressed in stipules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMĀIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-Binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001005; Myb DNA binding, Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                          STRAIN=cv. Columbia,
                                                                                                                                                                               ecotype Columbia.";
DNA Seq. 9:177-181(1998)
                                                                                                                                                                                                    Shikazono N., Tanaka A., Yokota Y., Wa
"Nucleotide sequence of the GLABROUS1
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                     GL1 OR AT3G27920 OR K16N12.17
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HSSP; P01103; 1POM.
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                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           67:483-493 (1991).
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9 61 MYB
62 112 MYB
205 212 POL
234 273 ASP
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234
273
                                                            Evol.
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                                                           18:1754-1763 (2001)
                                                                                                                                           CV.
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  Sato S., Nakamura
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MYB 2.
POLY-GLY.
ASP/GLU-RICH (ACIDIC
ASP/GLU-RICH (ACIDIC
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Pred. No.
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                                                                                                                                                                                                     Y., Watanabe H., Tano S.; BROUS1 gene of Arabidopsis
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   Tabata
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Best Local
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EMBL; AB006078; BAA86879.1; -.
EMBL; AF263690; AAL01215.1; -.
EMBL; AF263690; AAL01218.1; -.
EMBL; AF263694; AAL01219.1; -.
EMBL; AF263695; AAL01220.1; -.
EMBL; AF263695; AAL01221.1; -.
EMBL; AF263697; AAL01227.1; -.
EMBL; AF263697; BAB02538.1; -.
                   Salamini F
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P20026;
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CONFLICT
SEQUENCE
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PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-Binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001005
Pfam; PF00249; myb
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                                                                                   STRAIN=cv. Abyssinian 2231;
MEDLINE=89313655; PubMed=2664447;
                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                     01-FEB-1991
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              HORVU
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Sequence features of
                                         Marocco A., Wissenbach M., Salamini F., Rohde W.;
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                 Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                   Myb-related
                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991
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                                                                                                                                                                  NCBI_TaxID=4513;
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FUNCTION: REGULATES
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SM00717; SANT; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIHKLIGNRWSLIA 95
genes are transcribed in Hordeum vulgare and DNA binding domain of the myb oncoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 AA;
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(Rel. 17,
(Rel. 40,
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64
149
222
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oinding; 2.
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yta; Liliopsida; Poales; Poaceae; Pooideae;
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                                                               Becker D.,
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MYB 2.
MYB 2.
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GDV -> SDI (IN REF. 1).
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Pred. No.
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                                                             Paz-Ares J.,
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RESULT MYBPMAN ID MYBPMAN ID MY P2 AC P3 A
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Matches 12
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01-AUG-1992 (Rel
01-AUG-1992 (Rel
08-FEB-2003 (Rel
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                                                                                                                                                                                                                    Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
PACCAD clade; Panicoideae; Andropogoneae;
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X70877; CAA50222.1; -.
EMBL; X70877; CAA50224.1; -.
EMBL; S61506; S61506.
HSSP; P01103; 1POM.
                              MEDLINE=91271238; PubMed=2052542;
Grotewold E., Athma P., Peterson T.;
"Alternatively spliced products of the maize P gene encode proteins
with homology to the DNA-binding domain of myb-like transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAIZE
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PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
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SMART; SM00717; SANT;
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InterPro; IPR001005; Myb_DNA_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Probable) TISSUE SPECIFICITY: GERMINATING SEED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: POSSIBLE
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12; Conserv
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                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSLIAGRLPGRT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSLIAGRLPGRT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genet.
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267 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abyssinian
                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 23, Created)
(Rel. 23, Last sequence up
(Rel. 41, Last annotation
protein P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
112
29740 Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216:183-187(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2231; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSCRIPTION AY BE INVOLVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YB 1.
YB 2.
DBECEDCEBA847749 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
0.00011
                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta;
a; Poales; Poaceae;
e; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E TO AN
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RESULT
M3K4_MC
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Best Local S
Matches 9
                                                                                                                                                                                                                                                   InterPro; IPR001005; Myb_DNA_binding.
pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS00334; MYB 3; 2.
NICTION TO THE STORY OF THE STORY OF T
M3K4 MOUSE STANDARD;
OO8648; OO8649; O70124;
30-MAY-2000 (Rel. 39, Created)
                           MOUSE
                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                             TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M73028; AAA33500.1; -.
EMBL; M73029; AAA33501.1; -.
EMBL; Z11879; CAA77939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics 131:199-209(1992).
-!- FUNCTION: TRANSCRIPTION FACTOR POSTULATED TO BIOSYNTHETIC PATHWAY OF A FLAVONOID-DERIVED
                                                                                                                                 SEQUENCE
                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Insertional mutagenesis of the maize transposition of Ac.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Athma
                                                                                                                                                                                                                                      Alternative splicing
                                                                                                                                                                                                                                                Nuclear
                                                                                                                                                                                                                                                                                                            MaizeDB; 69181; -
                                                                                                                                                                                                                                                                                                                   MaizeDB; 69180; -.
                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (Probable) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLORAL TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2.
                                                                                                                                                                                                                                                                                                                                             A39697; A39697.
B39697; B39697.
; P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P27898-1; Sequence=Displayed;
                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P27898-2; Sequence=VSP_003301, v
MILARITY: Contains 2 Myb-like domains.
                                                                                              l Similarity
9; Conserv
                                                                                                                                                                                                                                              protein; DNA-binding; Repeat;
                                                                        LGNRWSLIA 92
                                                              LGNRWSLIA 93
                                                                                                                                                                                                                                                                                                                             T01590; -.
T01591; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grotewold
                                                                                                                                  399
                                                                                                                                                                                            178
305
89
                                                                                              Conservative
                                                                                                                                                  153
                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1317315;
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112
181
311
352
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                                                                                            43756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peterson
                                                                                                                                 MW;
                                                                                              Score 9; DB 1; Pred. No. 0.2 0; Mismatches
                                                                                                                                                                                                             MYB 1.
MYB 2.
POLY-ALA.
                                                                                                                                                                          POLY-LEU.
WSLIASHEGRTDNEIKNYWNSHLSRQIHTYRRKYTAGEDD
TAIALDWSKLOSADRRRGGRTPG -> RHLMIEADYSBPST
VRCLERGALAYLTLPRQSPFQTARITYDRIGSALLRSVRFC
                                                                                                                                                         /FTId=VSP_003301.
                                                                                                                                         /FTId=VSP_003302
                   PRT;
                                                                                                                                 EE025B00A44CF5D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
::
                                                                                                                                                 (In isoform Short).
                                                                                                      DB 1;
o. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ש
                                                                                                                                                                                                                                              Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene by intragenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSP_003302;
                                                                                              0;
                                                                                                                Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO REGULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIGMENT IN CERTAIN
                                                                                               Indels
                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                              Gaps
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NP_BIND
BINDING
ACT_SITE
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28-FEB-2003 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase 4 (EC (MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK 4).
MAP3K4 OR MEKK4.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Ectoplacental cone; MEDLINE-97422605; PubMed=9268631; Schweifer N., Valk P.J., Delwel R., Cox R., Meier-Ewert S., Lehrach H., Barlow D.P.; "Characterization of the C3 YAC contig from 17 and analysis of allelic expression of gen
                                                                           DOMAIN
                                                                                                                                                                          Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement into tremoved. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENOMICS 43:285-297(1997).
-!- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, BUT NOT THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4
                                                                                                                                                                                                                                                                                                                                                                              EMBL; U66240; AAC08286.1;
HSSP; P24941; 1HCL.
MGD; MGI:1346875; Map3k4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 363-1049 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of a novel mirogen-accivation MEKK4, that selectively regulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerwins P., Blank J.L., Johnson G.L., "Cloning of a novel mitogen-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97236778; PubMed=9079650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                Transferase;
Alternative :
                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the
                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: LOCALIZED IN PERINUCLEAR STRUCTURES, PROBABLY GOLGI-ASSOCIATED VESICLES ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKELETAL MUSCLE, KIDNEY, TESTIS FOLLOWED BY HEART BRAIN AND LUNG. LOW EXPRESSION WAS FOUND IN SPLEEN.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=008648-2; Sequence=VSP_004885; TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGH EXPRESSION WAS FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND MAP2K6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                      U85607; AAC53; U85608; AAC53; U66240; AAC08; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=008648-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem.
7e splicing.
1178 1182
1332 1590
1338 1346
1361 1361
1452 1452
                                                                                                                                                       Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC53126.1; -.
AAC53127.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC08286.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272:8288-8295(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing; Named isoforms=2;
     PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A AND
                                                                                                      POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase kinase kinase,
c-Jun amino terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rom proximal mou
genes flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Francis F.,
                                                                                                                                                       ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.7.1.-)
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e imprinted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., ALTERNATIVE SI
TISSUE-Fetal liver, and Skeletal r
MEDLINE-97449143; PubMed-9305639;
Takekawa M., Posas F., Saito H.;
"A human homolog of the yeast Ssk."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M3K4 HUMAN STANDARD; PRT; 1607 AA. 09Y6F4; Q92612; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-GEB-2003 (Rel. 41, Last annotation update) (MSC) (MSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMUH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Prediction of the coding sequences of unidentified human The coding sequences of unidentified human and the coding sequences of 80 new genes (KIAA0201-KIAA0280) danalysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAP3K4 OR MAPKKK4 OR MEKK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97191544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 68-1607 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 16:4973-4982(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTK1, mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                  ISOId=Q9Y6R4-2; Sequence=VSP 0048B4; TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN HEART, PLACENTA, SKELETAL MUSCLE AND PANCREAS, AND AT LOWER LEVELS IN OTHER TISSUES.
                                                                                                                                                                                                                DOMAIN: THE N-TERMINAL NON-CATALYTIC DOMAIN (1-606) CONTAINS A ESSENTIAL DOMAIN FOR THE DOMINANT-INHIBITORY EFFECT. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SER/THR FAMILY KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, I THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND MAP2K6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 LILRLHKL 540
                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9Y6R4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seki N., Ishikawa K.-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 8; DB 1
%; Pred. No. 8.7
0; Mismatches
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/FTId=VSP 004885.
SL -> NS (IN REF. 2).
T -> A (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Named isoforms=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohira M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                      There are no restrictions of as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                          . Usage by and for http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawarabayasi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 9
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Best Local :
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SEQUENCE
                                                       STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=9535630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D. Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
ACT_SITE
                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Nitrate/nitrite response regulator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodom; PD000001; Prot_kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS00100; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF002715; AAB68804.1; -.
EMBL; D86968; BAA13304.1; -.
PIR; T03022; T03022.
HSSP; P24941; 1HCL.
                                                                                                                                                                                                               Haemophilus influenzae.
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                       01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0006950; P:response to stress; InterPro; IPR000719; Prot kinase. InterPro; IPR002290; Ser_thr_pkinase.
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          Science 269:496-512(1995)
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                                         NARP OR HI0726
                                                                                                                                                                                                                                                                                                                 P44845;
                                                                                                                                                                                                                                                                                                                              NARP_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M :
                                              Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative sp.
                                  "Whole-genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0004709; P:MAP kinase kinase kinase activity; GO:0000186; P:activation of MAPKK; TAS. GO:0007254; P:JNK cascade; TAS.
FUNCTION: COULD ACTIVATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602425;
                                                                                                                                                                                                                                                                                                                                                                                         542 LILRLHKL 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conserv
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                                  random sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 004884.
K->R: LOSS OF ACTIVITY.
I -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                 PRT;
                                   and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
EXPRESSION OF
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                                                                                                                                                                                                                                                                   ion update)
protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (in isoform B)
                                                                                                                                                                                                                                                                                                                                 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
o. 8.8;
                                                                                                                                Clayton R.A., Kirkness E.F.
Dougherty B.A., Merrick J.M.
                                   of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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 A FORMATE DEHYDROGENASE
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RESULT 10
NARP_ECOLI
ID NARP_ECOLI
7 P31802;
7 -JUL-196
  REAR RELEASE OF THE R
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Best Local Similarity
Matches 7; Conserv
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InterPro; IPR001789; Response_reg.
Pfam; PF00072; response_reg; 1.
Pfam; PF00072; response_reg; 1.
PRINTS; PR00038; HTHLUXR.
PRODOM; PD000307; HTH LuxR; 1.
PRODOM; PD0003039; Response_reg; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00428; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate/nitrite response regulator protein narp.
NARP OR B2193.
                                                                                                                                                  "Dual response regulators (NarL and NarP) interact with dual sensors (NarX and NarQ) to control nitrate- and nitrite-regulated gene expression in Escherichia coli K.12.";
J. Bacteriol. 175:3259-3268(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00622; HTH LUXR FAMILY; 1.
PROSITE; PS50110; RESPONSE REGULATORY; 1.
Transcription regulation; Activator; Repressor; DNA-binding;
ATP-binding; Phosphorylation; Sensory transduction; Complete;
DOMALN
6 12
POSPHORYLATION; REGULATORY.
MOD RES
57 57
PHOSPHORYLATION (BY SIMILARITY).
DNA_BIND 166 185 H-T-H MOTIF (BY SIMILARITY).
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                                                                                                                                                                                                                                                    MEDLINE=93273691; PubMed=8501030; Rabin R.S., Stewart V.;
Submitted (OCT-1993) to
                                             Richterich P., Lakey
                                                                          STRAIN=K12
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P10957; 1RNL.
TIGR; HI0726; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                          Church G.M.
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REDUCTASE (FRDABCD) C
- SIMILARITY: Contains
- SIMILARITY: BELONGS T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long as its content and this statement is not removed. Usage by an requires a licence
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                                                                            BHB2600;
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the EMBL/GenBank/DDBJ databases
                                               Gryan G., Jaehn L., Mintz L., Robison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0B72119BEC4906C7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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PSB2 CEPAL

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Best Local S
Matches 7
                                                                               PSB2 CRYNE
Q00826;
16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO0448; REC; 1.

SMART; SMO0448; REC; 1.

PROSITE; PS00622; HTH LUXR FAMILY; 1.

PROSITE; PS00622; HTH LUXR FAMILY; 1.

PROSITE; PS00622; HTH LUXR FAMILY; 1.

Transcription regulation; Activator; Repressor; DNA-binding; Transcription regulation; Formory transduction; ATP-binding; Phosphorylation; Sensory transduction; Nitrate assimilation; Complete proteome.

Nitrate assimilation; Complete proteome.

RESPONSE REGULATORY.

PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00038; HTHLUXR.

ProDom; PD000307; HTH LuxR; 1.

ProDom; PD000039; Response_reg;

SMART; SM000421; HTH LUXR; 1.

SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a copyrender the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L11273; AAA24200.1; -.
EMBL; U00008; AAA16411.1; ALT_INIT.
EMBL; AE000309; AAC75253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D Mau B., Shao Y.;
                                                                 Probable
                                                                                                                                                                      CRYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00196; GerE; 1.
Pfam; PF00072; response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EcoGene; EG11527; narP.
InterPro; IPR000792; HTH LuxR.
InterPro; IPR001789; Response_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A40584; A40584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS PROTEIN ACTIVATES THE EXPRESSION OF THE NITRATE REDUCTASE (NARGHJI) AND FORMATE DEHYDROGENASE-N (FDNGHI) OPERONS AND REPRESSES THE TRANSCRIPTION OF THE FUNARATE REDUCTASE (FRDABCD) OPERON IN RESPONSE TO A NITRATE/NITRITE INDUCTION SIGNAL TRANSMITTED BY EITHER THE NARX OR NARQ PROTEINS.

SIMILARITY: Contains 1 response regulatory domain.

SIMILARITY: BELONGS TO THE LUXE/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 response regulatory domain.
SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL REGULATORS. SIMILAR TO THE NARL PROTEIN.
                                                                                                                                                                                                                                                                         110
                                                                                                                                                                                                                                         191 NLLRKLN
                                                                                                                                                                                                                                                                                                       l Similarity
7; Conserv
                                                                   proteasome
                                                                                                                                                                                                                                                                       NLLRKLN 116
                                                                                                                                                                                                                                                                                                                                                                           171
215 AA;
                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
steasome subunit beta type 2 (EC 3
                                                                                                                                                                                                                                                                                                         Conservative (
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23575 MW;
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Pred. No. 15;
0; Mismatches
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H-T-H MOTIF (BY SIMILARITY).
; C7121668E3130956 CRC64;
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                                                                                                                                                                                                                                                                                                                DB
15;
                                                                                                                                                      224
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                                                                   3.4.25.1).
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yhew G.F.,
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MYB3_MA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                  LT 12
MAIZE
"Multiple genes are transcribed in Hordeum vulgare an carry the DNA binding domain of the myb oncoproteins. Mol. Gen. Genet. 216:183-187(1989).

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. NCBI_TaxID=4577;
                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Las
28-FEB-2003 (Rel. 41, Las
Myb-related protein Zm38.
Lea mays (Maize).
                                                                            MEDLINE=89313655; PubMed=2664447; Marocco A., Wissenbach M., Becker D., Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                   MYB3_MAIZE
P20025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000243; Proteasome_B.
InterPro; IPR001353; Proteme_protease.
Pfam; PF00227; proteasome; 1.
PROSITE; PS00854; PROTEASOME_B; FALSE_NEG.
Proteasome; Hydrolase; Protease.
SEQUENCE 224 AA; 25239 MW; ABEEF03E761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L40028; AAB06582.1;
HSSP; P22141; 1RYP.
MEROPS; T01.984; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang Y.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96239006; PubMed=8675296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ifice remittees the statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ect. Immun. 64:1977-1983(1996).

EVINCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP; DEPENDENT PROTEOLYTIC ACTIVITY (BY SIMILARITY).

CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolytic pathway.
SUBUNIT: THE PROTEASOME
SUBUNITS WHICH FORM A HI
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic and nuclear SIMILARITY: Belongs to peptidase family TIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specificity.
PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                160
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                LLRKCID
                                                                                                                                                                                                                                                                                                                                                                                                LLRKCID 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for virulence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penoyer L.A., Kwon-Chung K.J.; capsule gene of Cryptococcus neoformans, CAP64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORM A HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.6%;
                                                                                                                                                                                                                                                     Last
                                                                                                                                                                                                                                                                                    Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOSED OF AT LEAST 15
LY ORDERED RING-SHAPED ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                 255
                                                                                            Paz-Ares J.,
                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 224;
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                                                             and
                                                                                              Saedler
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                                                               Zea mays that
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MYB3 HORWI

ID MYB3

AC P2002

DT 01-JU

GN MYB2.

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GN MYB2.

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GO TITITI

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Best Local S
Matches 7
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TRANSPAC, T02959; -.

MaizeDB, 65994; -.

InterPro, IPR001005; Myb_DNA_binding.

Pfam; PF00249; myb_DNA-binding; 2.

SMART; SM00717; SANT; 2.

PROSITE; PS00037; MYB_1; 1.

PROSITE; PS00034; MYB_2; 1.

PROSITE; PS00034; MYB_3; 2.

Nuclear protein; DNA-binding; Repeat; Transcription regulation.

Nuclear protein; DNA-binding; Repeat; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYB3 HORVU
P20027;
01-FEB-1991
01-JUN-1994
16-OCT-2001
Myb-related
                                                                                                                                                                                                                                                                                                                                                     "Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the DNA binding domain of the myb oncoproteins.";
Mol. Gen. Genet. 216:183-187(198).

-i- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR IN RESPONSE TO AN EXTERNAL SIGNAL. MAY BE INVOLVED IN THE REGULATION OF FLAVONOID
                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Abyssinian 2231; TISSUE-Leaf; MEDLINE-94035190; PubMed-8220488; Missenbach M., Ueberlacker B., Vogt F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HORVU
                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marocco A., Wissenbach M., Becker D., Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Abyssinian 2231;
MEDLINE=89313655; PubMed=2664447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 35-302 FROM N.A. STRAIN=cv. Abyssinian 2231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myb genes from Hordeum vulgare: tissue-specific chimeric Myb promoter/Gus genes in transgenic tob Plant J. 4:411-422(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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HSSP; P01103; 1POM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4513;
                                                                                                                                                                                                                                        SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear ()
TISSUE SPECIFICITY: GERMINATING
                                                                                                                                                                                                                                                                                                                                      BIOSYNTHESIS.
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7; Conserv
                                                                                                                                                                                                                                                                 ROOT
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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27568 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26AAADC8B0633E06 CRC64;
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WG SEED AND
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paz-Ares J.,
                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                               There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becker D.,
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                                                                                           Usage
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EMBL; X70881; CAA50226.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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P37526;
01-OCT-1994
01-OCT-1994
28-FEB-2003
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DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96051385; PubMed=7584024;
Ogasswara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00334; MYB 2; 1.

PROSITE; PS50090; MYB 3; 2.

Nuclear protein; DNA-Dinding; Activator; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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S31818; S31818.
; P01103; 1POM.
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Tacconi E., Takagi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
(Rel.
(Rel.
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64
259
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114
259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No
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; 89017418C3631599 CRC64;
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MYB 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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"Molecular cloning and mapping
dehydrogenase (MDH1).";
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Hypothetical protein; Complete proteome.
SEQUENCE 315 AA; 37978 MW; E9BEZ5481FA13519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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| 10 3.6 46 10 QBLCGS 110 3.6 47 10 QBLCGS 110 3.6 247 10 QBLCGS 110 3.6 243 10 QBTCGS 110 3.6 243 10 QBTCGS 110 3.6 286 10 QBH257 110 3.6 287 10 QBH259 110 3.6 287 10 QBH259 110 3.6 293 10 Q4DM4 110 3.6 293 10 Q4DM5 110 3.6 293 10 Q94DM5 110 3.6 317 10 QBF259 110 3.6 317 10 QBF259 110 3.6 317 10 Q9FD3 110 3.6 342 10 Q9FD3 110 3.6 342 10 Q9FD3 110 3.6 341 10 Q9FD3 110 3.6 371 10 Q9FD3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 12 4.4 43 10 Q9SQA2 12 4.4 45 10 Q9SQA2 12 4.4 25 10 Q9SA2 12 4.4 23 10 Q9SA2 12 4.4 23 10 Q9SA2 12 4.4 24 10 Q9SA2 12 4.4 24 10 Q9SA2 12 4.4 26 10 Q9SA2 12 4.4 26 10 Q9SA2 12 4.4 26 10 Q9SA2 12 4.4 263 10 Q9SA2 13 4.4 263 10 Q9SA2 14 264 10 Q9SA2 15 4.4 265 10 Q9SA2 16 4.4 267 10 Q9SA2 17 4.4 282 10 Q9SA2 18 4.4 282 10 Q9SA2 19 4.4 283 10 Q9SA2 11 4.0 267 10 Q9SA2 11 4.0 268 10 Q9SA2 11 4.0 268 10 Q9SA2 11 4.0 269 10 Q9SA | 3 13 4.7 376 10 Q9SBF7<br>4 13 4.7 388 10 Q40920<br>5 12 4.4 35 10 Q8GUX0                             |
| 10 3.6 46 10 Q8L6S2 Q816S2 Q816S2 Q816S2 Q816S1 Q816S2 Q916S2 Q91 | 12 4.4 43 10 QSQQ24 QSQQ25 QSQ | 3 13 4.7 376 10 Q9SBF7<br>4 13 4.7 388 10 Q40920<br>5 12 4.4 35 10 Q8GUX0                             |
| 10 3.6 46 10 QBLGS2 QB1682 QB1 | 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 3 10 095085 12 4.4 4 18 10 095085 12 4.4 4 18 10 095085 12 4.4 1 18 10 095085 12 4.4 1 18 10 095085 12 4.4 1 18 10 095085 12 4.4 2 18 10 095085 12 4.4 2 18 10 095085 12 4.4 2 18 10 095085 12 4.4 2 23 10 095085 12 4.4 2 23 10 095085 12 4.4 2 24 10 095085 12 4.4 2 24 10 095085 12 4.4 2 25 7 10 095985 12 4.4 2 25 7 10 095985 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095085 12 4.4 2 26 10 095087 12 4.4 2 26 10 095087 12 4.4 2 26 10 095087 12 4.4 2 26 10 095087 12 4.4 2 26 10 095087 11 4.0 26 10 095087 11 4.0 26 10 095087 11 4.0 26 10 095087 11 4.0 26 10 095087 11 4.0 26 10 095087 11 4.0 26 10 095087 11 4.0 26 10 095087 11 4.0 3.6 42 10 095085 11 4.0 3.6 42 10 095085 11 4.0 3.6 42 10 095085 11 4.0 3.6 42 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 3.6 43 10 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 095085 11 4.0 09508 | 3 13 4.7 376 10 Q9SBF7 4 13 4.7 388 10 Q40920 Q40920 pices 5 12 4.4 35 10 Q8GUX0 Q8GUX0 Q8GUX0 pices  |
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| $\begin{array}{c} 6.22 \times 2.22 \times 1.22 \times 1.$ |                                                                                                                                  |
| 10 Q8VZ77<br>10 Q93X77<br>11 Q93X77<br>12 Q93X77<br>13 Q93X77<br>14 Q8S3R9<br>17 Q8LV04<br>18 Q8S3R9<br>19 Q8S3R9<br>10 Q8S3R1<br>10 Q8S3R1<br>11 Q9Z4C1<br>11 Q9Z4C1<br>12 Q9Z4C1<br>13 Q8UTNS<br>14 Q9UTNS<br>15 Q8UTNS<br>16 Q8UTNS<br>17 Q8UTNS<br>17 Q8UTNS<br>18 Q8UTNS<br>19 Q8TS<br>10 Q8SS<br>11 Q8SS<br>11 Q8SS<br>12 Q8UTNS<br>13 Q8HB01<br>14 Q8SS<br>15 Q8UTNS<br>16 Q8UTNS<br>17 Q8UTNS<br>17 Q8UTNS<br>18 Q8UTNS<br>19 Q9Y802<br>10 Q8SS<br>11 Q8SS<br>11 Q8SS<br>12 Q8UTNS<br>13 Q8GUNS<br>14 Q9SS<br>15 Q8GUNS<br>16 Q9Y808<br>17 Q8GUNS<br>18 Q8GUNS<br>19 Q8GUNS<br>10 Q8GUNS<br>11 Q8GUNS<br>11 Q8GUNS<br>12 Q9SS<br>13 Q8GUNS<br>14 Q9SS<br>16 Q9SS<br>17 Q8GUNS<br>17 Q8GUNS<br>18 Q8GUNS<br>19 Q8GUNS<br>10 Q9SS<br>11 Q9SS<br>11 Q9SS<br>11 Q9SS<br>12 Q9SS<br>13 Q9SS<br>14 Q9SS<br>15 Q9SS<br>16 Q9SS<br>17 Q9SS<br>17 Q9SS<br>18 Q9SS<br>18 Q9SS<br>19 Q9SS<br>10 Q9SS<br>11 Q9SS<br>11 Q9SS<br>11 Q9SS<br>12 Q9SS<br>13 Q9SS<br>14 Q9SS<br>15 Q9SS<br>16 Q9SS<br>17 Q9SS<br>17 Q9SS<br>18 Q9SS<br>18 Q9SS<br>19 Q9SS<br>10 Q9SS<br>10 Q9SS<br>10 Q9SS<br>11 Q9SS<br>11 Q9SS<br>11 Q9SS<br>12 Q9SS<br>13 Q9SS<br>14 Q9SS<br>15 Q9SS<br>16 Q9SS<br>17 Q9SS<br>17 Q9SS<br>18 Q9SS<br>18 Q9SS<br>19 Q9SS<br>10 Q9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                  |
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| Q8vz/1<br>Q9vxx5<br>Q9vxx5<br>Q9vxx5<br>Q9vxx5<br>Q9vxx5<br>Q8ij52<br>Q8ij52<br>Q8ij52<br>Q8ij52<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q8ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9ij76<br>Q9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Q9er<br>Q9fi<br>Q9dd<br>Q9zw<br>Q8wvc<br>Q8wvc                                                                                   |
| 50 plass pla                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :q3 mus .a4 ara lk5 car .f9 cuc .3 homo                                                                                          |
| Q8vz70 arabidopsis Q93x77 malus domes Q93x77 malus domes Q93x77 malus domes Q93x75 malus domes Q93x75 malus domes Q94x25 drosophila Q8s3z9 oxyza sativ Q1526 saccharomyc Q58474 pyrococcus Q81y52 plasmodium Q84y243 matbadopsis Q81y26 arabidopsis Q81370 spinacia ol Q4476 caenorhabdi Q8495 human immun Q80x175 human immun Q80x175 trypanosoma Q67811 aquifex aeo Q9507 drosophila Q84812 chlasmodium Q8138 plasmodium Q8148 cryptococcu Q8166 oxyza sativ Q91027 arabidopsis Q81724 plasmodium Q81480 plasmodium Q81481 plasmodium Q81493 plasmodium Q99387 banana mild Q81476 drosophila Q81478 dryptococcu Q81478 plasmodium Q81239 plasmodium Q99387 banana mild Q99387 banana                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Q9erq3 mus musculu<br>Q9fia4 arabidopsis<br>Q9ddk5 carassius a<br>Q9zwf9 cucumis mel<br>Q8wvc3 homo sapien<br>Q947f0 malus domes |

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Q9M714;
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                                                                                                        "Molecular analysis of the anthocyanin2 in the evolution of flower color."; Plant Cell 11:1433-1444(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SI-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMA EMBL; AF146709; AAF66734.1;
HSSP, P06876; 1MBK.
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Quattrocchio F., Wing
Mol J., Koes R.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Petunia.
                                                      InterPro; IPR001005; Myb_DNA_binding. Pfam; PF00249; myb_DNA-binding; 2. SMART; SM00717; SANT; 2.
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PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
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SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB-2; 1.
PROSITE; PS00334; MYB-3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 127 AA; 14789 MW; 58:
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Q9M721;
01-OCT-2000
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                                                                                    Petunia hybrida (Petunia).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol J., Koes R.;
"Molecular analysis of the anthocyanin2
in the evolution of flower color.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=cv. W22; TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petunia hybrida (Petunia).
Bukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; e
Asteridae; lamiids; Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An2 truncated protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4102;
                                                 NCBI_TaxID=4102;
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001005; Myb DNA binding Pfam: PF00249; myb DNA-binding; 2.
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                                                                                                                                                                                                                                                                   (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Petal limb;
6; PubMed=10449578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%;
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01-OCT-2000
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Q9M720;
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SMART; SM00717; SANT; 2.
PROSITE; PS00037.
                                                                                         PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 255 AA; 29007 MW;
                                                                                                                                                                                                                in the evolution of flower color.";

Plant Cell 11:1433-1444(1999).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
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                                                                                                                                                                                           EMBL; AF146703; AAF66728.1; HSSP; P06876; IMBK.
                                                                                                                                                                                                                                                                                                    STRAIN=cv. S9; TIS
MEDLINE=99380006;
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular analysis of the anthocyanin2 in the evolution of flower color."; Plant Cell 11:1433-1444(1999).
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Mol J., Koes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. V26; TISSUE=Petal limb; MEDLINE=99380006; PubMed=10449578; Quattrocchio F., Wing J., van der
                                                                                                                                                                                                                                                                                        Quattrocchio F., Wing J., van der Woude K.,
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                   Petunia integrifolia (Violet-flowered petunia) (Petunia inflata)
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                                                                                                                                                                              InterPro; IPR001005;
                                                                                                                                                                                                                                                                  Molecular analysis of the anthocyanin2
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                                                          Similarity
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               DEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
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DEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
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                                             Conservative
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                                                                                                                                                                                                                                                                                                                  TISSUE=Petal limb;
                                                                                                                                                                                                                                                                                                    PubMed=10449578;
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                                            Score 38; DB; Pred. No. 8.8
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Pred. No.
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                                                                                             48B18508AFD59C3F CRC64;
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dons; core eu
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Q9M716;
01-OCT-2000
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                                                        "Molecular analysis of the anthocyanin2 in the evolution of flower color."; plant Cell 11:1433-1444(1999).
                                                                                                                                    STRAIN=cv. W115; TISSUE=Pe
MEDLINE=99380006; PubMed=1
Quattrocchio F., Wing J.,
                                                                                                                                                                                                                                                                Petunia hybrida (Petunia).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
PROSITE; PS50090; MYB 3; 2.
               -!- SUBCELLULAR LOCATION: N
-!- SIMILARITY: CONTAINS 2
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           An2 truncated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF146707; AAF
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular analysis of the anthocyanin2 gene in the evolution of flower color."; Plant Cell 11:1433-1444(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quattrocchio F., Mol J., Koes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99380006; PubMed=10449578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. W44; TISSUE=Petal limb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An2 truncated protein
                                                                                                                     Mol J., Koes R.;
                                                                                                                                                                                                                                               NCBI_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petunia hybrida (Petunia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001005; Myb_DNA_binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA:
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                                                                                                                                                              TISSUE=Petal limb; PubMed=10449578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wing J., van der Woude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14817 MW;
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oliophyta; eudicotyledons; core eudicots;
Solanales; Solanaceae; Petunia.
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23,
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23,
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                                    NUCLEAR (BY SIMILARITY)
                   MYB-LIKE
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Last sequence update)
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No.
                     DOMAINS
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                                                                                                                                           Souer E.,
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P06876; 1MBK.

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PAVE RESULT OF THE PAVE READ OF THE PAVE
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Cfeasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
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Best Local :
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Q9FNV8;
01-MAR-2001
01-MAR-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thallana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00034; MYB_2; 1.
PROSITE; PS50099; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 129 AA; 15084 MW;
                                                                                                                                                             Nature 408:816-820(2000).

-!- SUBCELLULAR LOCATION: NUCLEAR (E
-!- SIMILARITY: CONTAINS 2 MYB-LIKE
EMBL; AY008379; AAG38381.; -
EMBL; AC020665; AAG52160.1; -
HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcription factor MYBI14 (Myb-related transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00249; myb_DNA-bInding; SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "MYB transcription f
Submitted (SEP-2000)
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                                                                              InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; SM00717; SANT; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                    analysis of chromosome 1 of the plant Arabidopsis
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0) to the EMBL/GenBank/DDBJ databases.
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RABOULT ON SERVICE CONTROL OF THE SERVICE CON
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WHEDLINE-210.6719; PubMed=11130712;

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

AN Hite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

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AN Hite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

AN Hite O., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

AN Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

AN Chung M.K., Conn L., Chao Q., Chen H., Feng J.-D., Fong B., Fujii C.Y.,

AN Chung M.K., Conn L., Conway A.B., Conway A.R., Fong B., Fujii C.Y.,

AN Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

AN Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

AN Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

AN Langin-Hoopper S., Lee A., Lee J.M., Lierz C.A., Li J.H., Li Y.-P.,

AN Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

AN Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

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AN Militscher J., Maranda M., Nguyen M., Rooney T., Rowley D.,

AN Militscher J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

AN Militscher J., Pham P.K., Rizzo M., Sointhwick A.M.,

AN Militscher J., Tambunga G., Toriumi M.J., Town C.D.,

AN Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Preguence and analysis of chromosome 1 of the plant Arabidopsis
                              Query Match
Best Local
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Best Local (
      Matches
                                                                                                                Pfam; PF00249; myb DNA-bīnding;
SMAXT; SM0717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB-2; 1.
PROSITE; PS00334; MYB-3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 246 AA; 28307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Nuclear protein. SEQUENCE 139 AA; 16007 MW;
                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FNV9;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative transcription
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Submitted (SEP-2000) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                           InterPro; IPR001005; Myb_DNA_binding
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Similarity
32; Conserv
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                                                                                                                                                                                                                                                                                                                                                            1MBK.
                                                                                                                                                                                                                                                                                               DNA-binding;
                              11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actor gene nomenclature in Arabidopsis to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No.
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      Score 32; DB; Pred. No. 2.1
0; Mismatches
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                                                                                                                         FF1C4B9176040D20 CRC64;
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1.3e-25;
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With E-21016719; PubMed-11130712;

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

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Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Fuljii C.Y.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Fuljii C.Y.,

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A Manitscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

A Militscher J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

A Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

A Sakano H., Tallon L. J., Tambunga G., Toriumi M.J., Town C.D.,

Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ZTC3;
Q9ZTC3;
01-MAY-1999
                                                                                                               EMBL; AC020665; AAC
HSSP; P06876; 1IDY
                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR (E

-!- SIMILARITY: CONTAINS 2 MYB-LIKE

EMBL; AF062915; AAC83637.1; --

EMBL; AF325124; AAC42002.1; --

EMBL; AC020665; AAC52164.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYB90 OR PAP2 OR T27F4.14.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcription factor (Production of anthocyanin pigment
protein) (MYB-related transcription factor, putative, 65699-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borevitz J.O., Xia Y., Blount J., "Activation Tagging Identifies a Phenylpropanoid Biosynthesis."; Plant Cell 12:0-0(2000).
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                        Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                      Nature 408:816-820(2000).
                                                                                                                                                                                                                                                      thaliana.
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MEDLINE=99056848; PubMed=9839469;
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B Regulator
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RESULT Q9ZTC7
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01-MAY-1999
01-MAY-1999
01-MAR-2003
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01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-cv. S6; TISSUE-Petal limb; McDLINE-99380006; PubMed-10449578; Quattrocchio F., Wing J., van der Woll T Vocan
                                                                               Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF146704; AAF66729.1; -.
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petunia integrifolia (Violet-flowered petunia) (Petunia inflata). 
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta 
Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots; 
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear protein. SEQUENCE 249 AA; 28100 MW;
                   SEQUENCE FROM N.A.
                                                                                                                                                                      MYB75
                                                                                                                                                                                       Putative transcription
                                                                                                                                                                                                                                                                                                  Q9ZTC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00037; MYB_1; 1.
PROSITE; PS50090; MYB_3; 2.
PNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol J., Koes R.;
"Molecular analysis of the anthocyanin2 in the evolution of flower color.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4103;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9M719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9M719
  STRAIN=cv. Columbia;
                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Cell 11:1433-1444(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001005; Myb_DNA_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                               42 RAGLNRCRKSCRLRWLNYLRPHIKRGDF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 AA;
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                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel.
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Conservative 0;
                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%;
                                                                                                                                                                                       tactor
                                                                                                                                                                                                       10, Created)
10, Last sequence update)
23, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s; Pred. No. 2.1.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      der Woude
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E4626F08B07071AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                  212
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                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
. 3.9e-21
                                                                                                     Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                    Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9e-21;
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                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of petunia
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Best I
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01-MAR-2003
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000314; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear proteit
SEQUENCE 248 AA; 28469 M
                                                                                                                         rederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi.H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin (Chiou J., Choi E., Dunn P., Gonzalez A., Howng B., Kim C., Koo T., Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Pham P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M., Vaysborg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL, AR32513; AAG09100.1; -.
EMBL, AC009323; AAG09100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene family from Arabidopsis thaliana.";
Plant J. 16:263-276(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF062908; AAC83630.1;
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HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kranz H.D.,
Petroni K.,
Tonelli C.,
                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia-0;
Borevitz J.O., Xia Y., Blount J.,
"Activation Tagging Identifies a (
Phenylpropanoid Biosynthesis.";
Plant Cell 12:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                              PAPI OR F25P12.92.

PAPI OR F25P12.92.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00037; MYB_1; 1.
PROSITE; PS000334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 212 AA; 24508 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Production of anthocyanin pigment 1 protein (Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FE25;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9FE25
                                                                      Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                HSSP; P06876; 1IDY
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tactor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Towards functional characterisation of the members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99056848;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                  InterPro; IPR001005; Myb DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLGNRWSLIAGRLPGRTANDVKNYWNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urzainqui A., Bevan M., Ma
Paz-Ares J., Weisshaar B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Denekamp M., Greco R., Jin H., Leyva
Urzainqui A., Bevan M., Martin C., Sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9839469;
 28469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.9%;
              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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 B86103A9AB5CF442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                Conserved MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
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                                                                                                                                                                                                                                                                                                                                               Regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α.,
                                                                                                                                                                                                                                                                                                                                                               c.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription
                                                                                                                                                                                                                                   £ E., ...
C., Koo T.,
                                                                                                                                                                                                                                               N.F.,
E., Chin C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT
Q8H262
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Best Local S
Matches 27
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Best Local
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Q94FG4;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2003 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Myb-11ke transcription fe
Gossypium herbaceum.
                                                                                                                                                                             01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein.
NON TER 1
SEQUENCE 179 AA
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00249; myb DNA-bInd:
SWART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF377306; AAK58019.1; -
InterPro; IPR001005; Myb DNA binding.
InterPro; IPR001005; Myb DNA-binding; 2.
           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                              eurosids II; Malvales;
NCBI_TaxID=47615;
                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypioides.
                                                                                                                                         Gossypioides kirkii.
                                                                                                                                                         MYB3.
                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Myb-like transcription factor 3 (Fragment).
                                                                                                                                                                                                                Q8H262;
                                                                                                                                                                                                                           Q8H262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "PCR-mediated recombination in a polyploid plant."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=34274;
SEQUENCE
                              Plant Mol.
                                            cotton."
                                                                 Cedroni
                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cronn R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                      "Evolution
           AY115511;
rer 1
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27; Conserv
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                                                                  3.F
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                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                  DLILRLHKLLGNRWSLIAGRLPGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGNRWSLIAGRIPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cedroni M., Haselkorn T.,
                               Biol.
                                                     and
                                                                                                                                                                                                                                                                                                                                                                       179 AA;
 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.9%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                           PRELIMINARY;
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                                                    Cronn R.C., d expression
                                                                  Cronn
                    AAN28279.1; -.
                               0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                        20830 MW;
 20967 MW;
                                                                                                                                                                                                                                                                                                                                      9.1%;
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19,
23,
                                                     Adams
of MYI
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Last annotation update)
or Myb 3 (Fragment).
                                                                                                                                                                                                                                                                                                                            °,
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                                                                                                                                                                                                                                                                                                                                      Score 25;
Pred. No.
                                                       MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                        CAA70C42F7CC9A8F CRC64;
 OFOA0FDE13250F7D CRC64;
                                                                  ×.۲.,
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osborne C., Wendel J.F.;
                                                                                                                                                                                                                           181
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                                                     Wilkins T.A.
s in diploid
                                                                                                                                                                                                                                                                                                                                      DB 10;
4.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
4.5e-20
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                                                    ., Wendel J.F.; and polyploid
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RESULT 15
Q94FG5
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Search completed: January 29, 2004, 20:21:09 Job time : 70 secs
                                                                                                                                             Query Match 9.1%; Score 25; DB 10; Length 184; Best Local Similarity 100.0%; Pred. No. 4.7e-18; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARI'
-!- SIMILARITY: CONTALNS 2 MYB-LIKE DOMAINS.
EMBL; AF377305; AAKS8018.1; -.
InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS00039; MYB 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Haselkorn T., Osborne C., Wendel J.F.,

"PCR-mediated recombination in a polyploid plant.";

"PCR-mediated recombination in a polyploid plant.";

Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.

Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                           Nuclear protein.
NON TER 1
SEQUENCE 184 A/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q94FG5 PRELIMINARY; PRT; 184 AA.
Q94FG5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myb-like transcription factor Myb 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29730;
                                                                      75 DLILRLHKLLGNRWSLIAGRLPGRT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 DLILRLHKLLGNRWSLIAGRLPGRT 88
                                                                                                                                                                                                                           184 AA; 21435 MW; FEEDB20F1E3E407A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 25; DB 10; illarity 100.0%; Pred. No. 4.6e-18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 181;
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                                                                                                                                                 0;
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